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COVID-19 Variant Surveillance in the Republic of Korea

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Abstract

Coronavirus disease (COVID-19) variants originating from the United Kingdom (UK), South Africa, and Brazil have recently spread throughout the world, and these variants are known to be different from non-variants in their transmissibility and immune effect. Accordingly, the World Health Organization has recommended public health measures for variants and proposed working definitions of variants of concern (VOCs) and variants of interest (VOIs).

The Korea Disease Control and Prevention Agency (KDCA) has been regularly monitoring the genotype and mutations of SARS-CoV-2, the virus that causes COVID-19, through whole-genome sequencing analysis from the initial outbreak of COVID-19 in the Republic of Korea on January 20, 2020 to the present. As a result, 162 cases of VOCs originating from the UK (138), South Africa (18), and Brazil (6) and 61 cases of VOIs originating from California, USA (55), New York, USA (3) and the UK/Nigeria (3) were identified early, and the genomic information of the variants confirmed through surveillance were shared with the GISAID database for international collaboration. To cope with the continuing spread of COVID-19 variants, the KDCA is continuing to strengthen its surveillance system by expanding its analytical capacity. This report was intended to help establish countermeasures to prevent the spread of variants by providing information on the characteristics of variants occurring in the Republic of Korea and internationally, and by reporting the results of domestic surveillance.

Keywords: Coronavirus disease (COVID-19), Virus variant, Whole-genome sequencing analysis

Introduction

The cause of the mysterious cases of pneumonia that occurred in Wuhan, China, in December 2019, was found to be infectious disease by SARS-CoV-2 virus (COVID-19). COVID-19 has spread worldwide, and as of March 1, 2021, it has infected nearly 114 million people and killed almost 2.5 million people. SARS-CoV-2, the causative pathogen of COVID-19, is an RNA virus that continuously mutates in the process of proliferation and transmission. Since most mutations confer disadvantages to viral survival or do not affect the characteristics of the virus, they disappear quickly or do not lead to significant

changes in the behavior of the virus; however, certain variants contribute to increased transmissibility or differences in other characteristics, such as changes in pathogenicity.

With the continuous spread of the COVID-19 pandemic, several variants originating in the UK and South Africa have recently spread to various countries, and these variants have also been detected in the Republic of Korea (hereafter, Korea) among incoming international travelers. Variants can be identified through genetic analysis (principally whole-genome sequencing), and genetic information related to variants is being shared worldwide through Global Initiative on Sharing All Influenza (GISAID) database and PANGO Lineages [1,2]. The

GISAID defines and classifies SARS-CoV-2 into clades based on genetic variants and shares information on the clades of SARS-CoV-2 registered in each country. PANGO names SARS-CoV-2 lineages (UK variant: B.1.1.7, South Africa variant: B.1.351, etc.) based on the PANGOLIN program (Phylogenetic Assignment of Named Global Outbreak lineages), thereby providing information for genetics-based epidemiological surveillance and outbreak investigation.

The Korea Disease Control and Prevention Agency (KDCA) also analyzes the genetic characteristics of SARS-CoV-2 among confirmed COVID-19 cases in international travelers and large-scale domestic outbreaks using whole-genome analysis, monitors the influx of variants into Korea, and internationally shares the genomic sequences of isolated viruses through GISAID.

This report aims to present the trends and characteristics of COVID-19 variants and the KDCA's results of surveillance of COVID-19 variants in Korea, based on genetic analyses.

Classification of variants

On February 25, 2021, the WHO proposed definitions of variants of concern (VOCs) and variants of interest (VOIs) as part of recommendations for public health interventions against variants [3].

1. Variants of concern (VOCs)

A VOC is defined as a variants which are associated with (1) increase in transmissibility or detrimental change in COVID-19 epidemics; and (2) increase in virulence or changes in clinical disease presentation; (3) decrease in effectiveness of public health, diagnostics, vaccines, and therapeutics; or (4)

classification as a VOC by the WHO in consultation with the SARS-CoV-2 Virus Evolution Working Group. For VOCs, the WHO coordinates laboratory research through the research group and conducts rapid risk assessments, communication of relevant information between member states, and revisions of guidelines as appropriate.

2. Variants of interest (VOIs)

A VOI is defined as a variant with (1) a mutation in an amino acid that can show or induce different traits compared to the reference isolate; and (2) community transmission, multiple infection cases, a massive outbreak, or detection in many countries; or (3) classification as a VOI by the WHO through consultation with the research group.

3. WHO recommendations

Member states are encouraged to provide information on VOI- and VOC-related cases occurring in each country to the WHO and to share genetic information obtained in each country through sequencing surveillance of positive samples on public databases such as GISAID. Furthermore, the WHO recommends that member states conduct laboratory evaluations for diagnosis and trait analysis, such as antibody immune response, along with field investigations to understand the epidemiology of VOIs and VOCs, their virulence, and public health impact, or that member states request support from the WHO if implementing such measures is challenging.

Characteristics of VOCs

1. 501Y.V1

On December 14, 2020, Public Health England reported that a new variant was identified during an investigation into the spread of COVID-19 in the southeastern region of the UK. Through a retrospective analysis, the first outbreak of the UK variant was confirmed to have taken place on September 20, 2020, and since then, it has now been identified in 106 countries. This variant, named VOC202012/01 or 501Y.V1, belongs to GISAID clade GR, B.1.1.7 lineage [4]. Recently, as the outbreak of 501Y.V1 has expanded, GISAID reclassified 501Y.V1, which belongs to the GR clade, into a separate GRY clade (2021.3.2.). The 501Y.V1 variant is characterized by mutations of the spike (S) protein (H69/V70 deletion, Y145 deletion, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H) and partial mutations of NSP6 (S106/G107/F108 deletion). Therefore, a diagnostic reagent targeting the S gene deletion site may produce a false negative result, but is also used to screen for mutations.

The 501Y.V1 variant is 1.5 times more transmissible than earlier variants of SARS-CoV-2 and has spread rapidly around the world, becoming the dominant variant in the UK. It was confirmed to raise the risk of death by 1.65 times compared to the non-mutant variant. A 2- to 3-fold reduction in the neutralizing capacity of naturally acquired or vaccine-induced immunity was confirmed, but the vaccine is still considered to be effective against the 501Y.V1 variant, and it is known to have no significant influence on the efficacy of monoclonal antibody therapy, which acts on the receptor binding domain (RBD).

At the end of December 2020, in addition to the existing 501Y.V1 variant, a variant with the E484K mutation was detected in the UK, and it was named VOC202012/02.

2. 501Y.V2

On December 21, 2020, the Africa Centers for Disease Control and Prevention reported that the 501Y.V2 variant was proliferating and spreading in South Africa after the second wave in early November. The variant was confirmed to have been registered for the first time on October 8, 2020, and it has been detected in 56 countries. The 501Y.V2 variant, which belongs to the B.1.351 lineage of the GH clade, is characterized by K417N, E484K, and N501Y mutations located in the RBD of the S protein, and it is believed to have a different origin from the 501Y.V1 variant [5].

The 501Y.V2 variant is reported to have a 1.5-fold increase in transmissibility according to incidence-based analyses, although no significant increase in virulence has been confirmed. The S protein E484K mutation of 501Y.V2 is considered to have a notable association with immune evasion, and it was confirmed that neutralizing capacity was lost in 27%-48% of serum samples from naturally infected people in the recovery period, and the reduction in the neutralizing capacity of the Moderna and Pfizer vaccines was 8.6-fold and 6.5-fold, respectively, raising concerns regarding the effectiveness of the vaccines. Furthermore, it was confirmed that the efficacy of monoclonal antibody therapy was also significantly reduced.

3. 501Y.V3

On January 6, 2020, a new variant was identified in Japan from a traveler arriving from Brazil on January 2. The variant was initially identified in Brazil on December 4, 2020, and it has been detected in 29 countries. The 501Y.V3 variant, which belongs to the P.1 lineage of the GR clade, contains the E484K and N501Y mutations of the S protein RBD region, as is the case

for 501Y.V2 [6].

Despite the high antibody positivity rate (approximately 75% in October 2020) in Manaus, Brazil, the sharp increase in the number of patients in mid-December 2020 and the detection of this variant suggests the possibility of immune escape, manifesting as increased transmissibility and re-infection. Compared to non-mutant variants, the 501Y.V3 variant is reported to be 1.4-2.2 times more transmissible, but no effect on virulence has been reported. A 6.5-fold reduction in neutralizing capacity was observed in the serum of naturally infected people during the recovery period, and a 2.2- to 2.8-fold reduction in neutralizing capacity was reported in the serum of vaccinated people. The effectiveness of monoclonal antibody therapy was also found to be greatly reduced.

Characteristics of VOIs

1. 452R.V1 and B.1.526

In January 2020, it was reported that a virus with an L452R mutation of the S protein, which is different from the existing UK and South African variants, was spreading in northern and southern California, USA. The 452R.V1 variant, which belongs to the B.1.429/B.1.427 lineage of the GH clade, is characterized by mutations of the S protein (S13I, W152C, and L452R) and has been identified in 22 countries [7].

It has been suggested that L452R.V1 may have increased transmissibility based on case occurrence, but further research is needed regarding virulence. In particular, the L452R mutation of the S protein is considered to affect vaccines' efficacy, but further experimental studies and clinical efficacy evaluations are needed due to the lack of related research results other than

the experimental results of the reduced efficacy of monoclonal antibody therapy.

In addition, it was reported that a variant of the B.1.526 lineage including the E484K mutation of the S protein occurred in New York, USA, in February 2021 [8]. It is estimated that the transmission started in November 2020 from a variant identified in an AIDS patient infected with COVID-19 (August 2020), and the variant is characterized by six mutations of the S protein (L5F, D253G, E484K, and D614G). Risk assessment is difficult due to the lack of scientific evidence for transmissibility and virulence, but the possibility of antibody evasion capability, potentially leading to reduced effectiveness of monoclonal antibody therapy due to mutations of D253G and E484K located in the S protein RBD, has been suggested.

2. 484K.V3

February 16, 2021, Public Health England reported a new variant identified in the UK and Nigeria. The 484K.V3 variant, which belongs to the B.1.525 lineage of the G clade, is characterized by the E484K mutation of the S protein and has now been identified in 23 countries [9]. The B.1.525 variant also shares the E484K mutation found in 501Y.V2, P.1 variants, suggesting the possibility that it may evade the immune response.

Status of variant identification in Korea

Since the initial COVID-19 outbreak in Korea in January 2020, the KDCA has been regularly conducting whole-genome analyses to confirm the genotypes and mutations of SARS-CoV-2 spreading in Korea. As of March 1, 2021, a total of 3,426

cases (2,462 domestic cases and 964 imported cases; 3.8% of all confirmed cases in Korea) were analyzed. In particular, since the UK variant was first identified in Korea in December 2020, the KDCA has been continuing to expand its analytical capacity.

1. The variant surveillance system in Korea

In order to monitor the outbreak of variants in Korea, genetic analyses are performed on representative specimens of domestic cases, considering the necessity of epidemiological analyses of massive outbreaks and sporadic outbreaks by region. For cases in international travelers, genomic analyses are prioritized according to the KDCA's evaluation of the risk of each country based on the proportion of variants, countries where variants have been identified, and countries with community outbreaks, which can be identified on the GISAID database. In particular, in order to respond to the influx and spread of variants from abroad, the analysis of genetic mutations has been expanded to five regional response centers since February 2021, and partial genetic analysis targeting only the S gene is also performed to increase the analytical volume by rapidly deriving results. Genetic information on SARS-CoV-2 confirmed through surveillance is also shared on the GISAID database to actively participate in international collaboration on variants.

2. Domestic COVID-19 virus genotype analysis and mutation monitoring

As a result of whole-genome analyses of SARS-CoV-2 in domestic cases, a number of S and V clades were identified until April 2020. After the Itaewon club outbreak in May 2020, the GH clade (89.8%) became the dominant type in Korea (Figure 1). However, since the emergence of the UK variant (501Y.V1), the

proportion of the corresponding clade (GRY) increased from 1.3% in December 2020 to 5.7% in February 2021. Various clades have been identified in cases in international travelers, but overall, GH was confirmed to be the most common with 38.2%, followed by GR (34.0%), G (10.9%), and GRY (9.4%). In cases in international travelers and their contacts, the proportion of the GRY clade increased significantly from 8.3% in December 2020 to 41.8% (Figure 2).

From December 2020 to March 1, 2021, a total of 162 cases of VOCs were identified in Korea, including 138 cases of the 501Y.V1 variant, 18 cases of 501Y.V2, and 6 cases of 501Y.V3 (Table 1). In particular, since 15 cases of the 501Y.V1 variant were confirmed in December 2020, it has been steadily becoming more common, reaching 72 cases in February 2021. Of the 138 cases of 501Y.V1, 104 were confirmed in international travelers from 21 countries, including Hungary (28 cases), the UK (18 cases), Ghana (10 cases), the UAE (9 cases), Poland (9 cases), and Jordan (7 cases). Among the 18 cases of the 501Y.V2 variant related to international travelers, 17 were confirmed in travelers from 7 countries including Tanzania (7 cases), the UAE (4 cases), and South Africa (2 cases). All 6 cases of the 501Y.V3 variant were confirmed to have been imported from 3 countries: Brazil (4 cases), Canada (1 case), and Saudi Arabia (1 case) (Table 2).

L452R.V1, a VOI originating from California, US, has been found in 55 cases since December 2020, of which 23 cases were confirmed among visitors from the US (21 cases) and Mexico (2 cases). B.1.526, which originated in New York, USA, was confirmed in 3 US visitors in February 2021. In addition, the 484K.V3 variant was confirmed in travelers who entered the country in February 2021 from Nigeria (2 cases) and Sudan (1 case). Thus, the influx of various variants from overseas has been confirmed during the monitoring process since February.

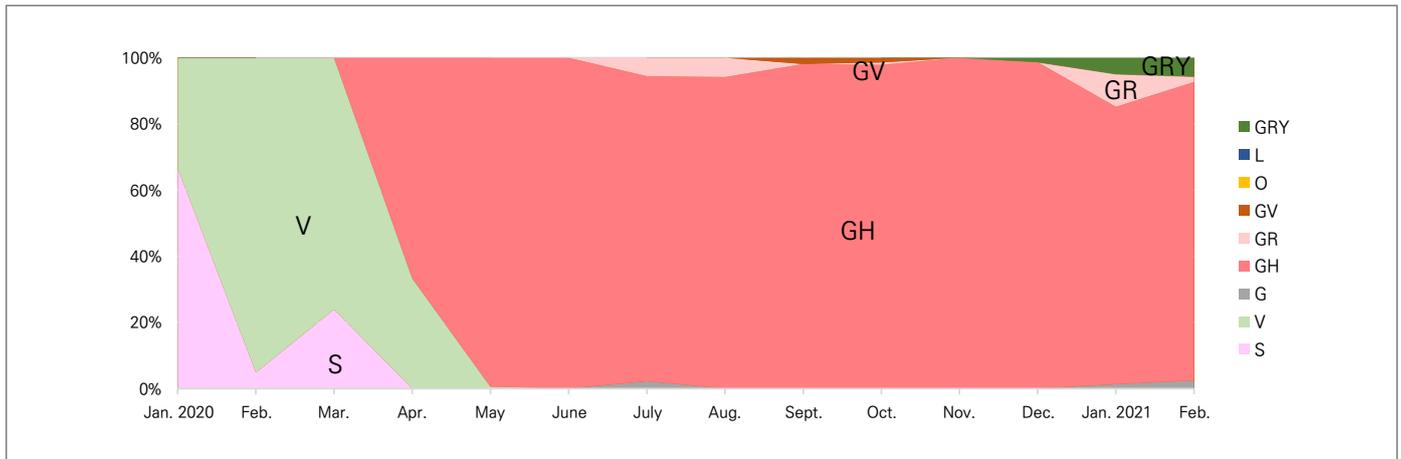


Figure 1. The distribution of the clades of COVID-19 virus in domestic cases

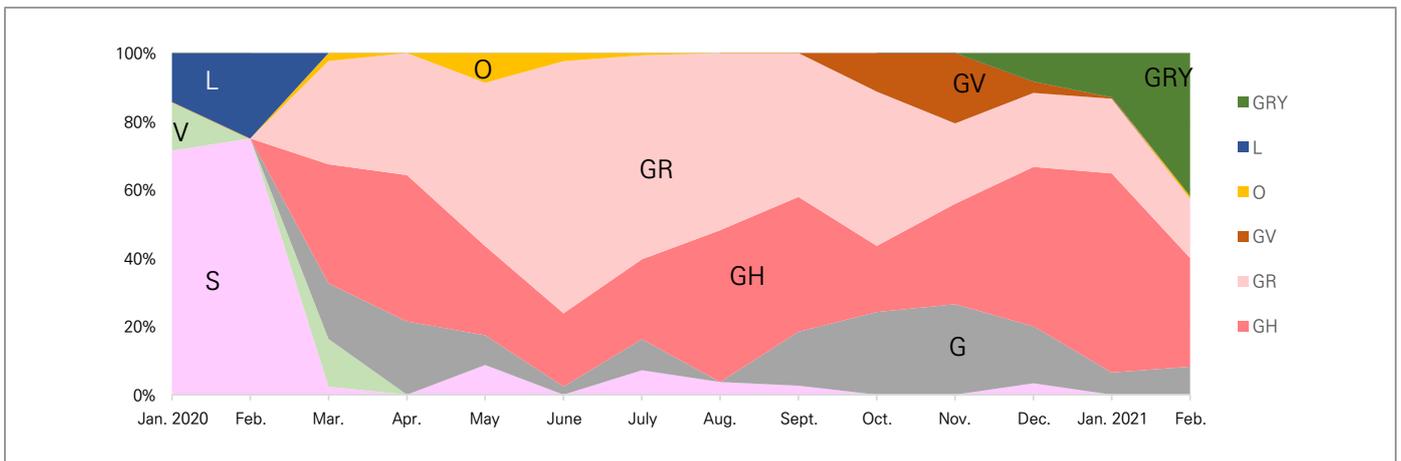


Figure 2. The distribution of the clades of COVID-19 virus in imported cases

Table 1. The occurrence status of COVID-19 variants in the Republic of Korea (As of March 1, 2021)

	No. of Samples	Variant of Concern (VOC)				Variant of Interest (VOI)			
		Total	501Y.V1	501Y.V2	501Y.V3	Total	452R.V1	B.1.526	484K.V3
Total	1,516	162 (10.7%)*	138 (9.1%)	18 (1.2%)	6 (0.4%)	61 (4.0%)	55 (3.6%)	3 (0.2%)	3 (0.2%)
Dec. 2020	495	16 (3.2%)	15 (3.0%)	1 (0.2%)	0 (0.0%)	14 (2.8%)	14 (2.8%)	0 (0.0%)	0 (0.0%)
Jan. 2021	551	67 (12.2%)	51 (9.3%)	10 (1.8%)	6 (1.1%)	20 (3.6%)	20 (3.6%)	0 (0.0%)	0 (0.0%)
Feb. 2021	470	79 (16.8%)	72 (15.3%)	7 (1.5%)	0 (0.0%)	27 (5.7%)	21 (4.5%)	3 (0.6%)	3 (0.6%)

* Confirmation rate of variants = (No. of variants / No. of Samples) × 100

Table 2. The routes in which the COVID-19 variants were identified in the Republic of Korea (As of March 1, 2021)

	Route	No. of Variants	Countries
Variant of Concern (VOC)	Imported	104	Total 21 countries: Hungary (28), United Kingdom (18), Ghana (10), UAE (9), Poland (9), Jordan (7), USA (5), Serbia (3), Pakistan (2), Iraq (2), Maldives (1), Nigeria (1), Norway (1), France (1), China(1), Slovakia (1), Libya (1), Ethiopia (1), Germany(1), Russia (1), Philippines (1)
	Imported	17	Total 7 countries: Tanzania (7), UAE(4), South Africa (2), Zimbabwe (1), Malawi (1), Zambia (1), USA (1)
	Imported	6	Total 3 countries: Brazil (4), Canada (1), Saudi Arabia (1)
Variant of Interest (VOI)	Imported	23	Total 2 countries: USA (21), Mexico (2)
	Imported	3	Total 1 country: USA (3)
	Imported	3	Total 1 country: Nigeria (2), Sudan (1)

Conclusion

Since December 2019, COVID-19 has continued to spread, and the magnitude of the outbreak of some variants is increasing. SARS-CoV-2 variants that can affect transmissibility or the immune response are spreading, and the WHO tentatively classifies variants as VOCs and VOIs and recommends public health interventions accordingly. Since the confirmation of the first COVID-19 case in Korea in January 2020, the KDCA has regularly analyzed the genetic characteristics of SARS-CoV-2 through whole-genome analysis, which led to the identification of VOCs (501Y.V1, 501Y.V2, and 501Y.V3) and VOIs (452R.V1, B.1.526, and 484K.V3). In order to respond to growing concerns about the influx of variants from abroad and the outbreak in Korea,

the KDCA has been continuing to strengthen the surveillance system by expanding its analytical capacity. However, since many characteristics of the new variants remain unknown, such as their transmissibility, pathogenicity, and virulence, it is necessary to clarify the characteristics of variants through laboratory, clinical, and epidemiological analyses.

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Conflict of Interest

No potential conflict of interest relevant to this article was

reported.

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① What was known?

The COVID-19 variants originating from the UK, South Africa, and Brazil have recently been spreading throughout the world, and it is known that they exhibit differences from existing forms of SARS-CoV-2, such as increased transmissibility and decreased immune response.

② What does this study add?

Through whole-genome analyses of COVID-19 in Korea, it was confirmed that the GH clade of SARS-CoV-2 is predominant. Since December 2020, VOCs originating from the UK, South Africa, and Brazil and VOIs from the US have been identified in Korea. Accordingly, the KDCA has been promoting enhanced surveillance by expanding its capacity for genetic analyses.

③ What are the implications?

In order to stem the influx and spread of variants in Korea, it is necessary to respond rapidly by strengthening the surveillance system for variants and establishing a scientific basis for responses by analyzing the characteristics of variants.

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Epidemiological and clinical characteristics of COVID-19 variants of concern in the Republic of Korea

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Abstract

From January 20, 2020 to March 1, 2021, a total of 90,029 cases of coronavirus disease 2019 (COVID-19) emerged after the first confirmed case was reported in Korea. In total, 162 patients with variants of concern (VOCs) have been confirmed since the first case of a VOC was confirmed in Korea in December 2020. The purpose of this paper is to analyze and share the epidemiological and clinical characteristics of VOC patients in Korea, as well as to offer suggestions on how to respond to VOCs, which can affect transmissibility and severity.

The epidemiological and clinical characteristics of 162 VOC cases in Korea were analyzed using initial and in-depth epidemiological investigation results reported through the Korea Disease Control and Prevention Agency (KDCA) COVID-19 information management system for managing confirmed patients (HIRAe).

The 162 VOC cases were divided into 3 groups: 501Y.V1, 501Y.V2 and 501Y.V3. There were 127 imported cases (78.4%) and 35 locally acquired cases (21.6%), and 106 male cases (65.4%) and 56 female cases (34.6%). The patients' average age was 36.4 years. People aged 30 to 39 accounted for 25.9% of cases. The majority of cases (105; 64.8%) were Korean nationals, and 100 cases (61.7%) were symptomatic at diagnosis. Thirty-seven cases (22.8%) involved mild respiratory symptoms without fever, and 27 (16.7%) had mild respiratory symptoms with fever. Most symptoms of VOC patients in Korea were mild, but 5 patients with the 501Y.V1 variant (the variant originating from the United Kingdom) were severe/critical (including 1 death). The rate of severe/critical symptoms was 3.09%, and the fatality rate was 0.6%.

However, since research on VOCs is continuing worldwide and the number of VOCs detected in Korea is increasing, it is important to establish a strategy for managing patients with variants through ongoing monitoring and analysis.

Keywords: Covid-19, Variant of Concern (VOC), Clinical characteristic

Introduction

In total, 93,217,287 cases of coronavirus disease-19 (COVID-19), which emerged in Wuhan, Hubei Province, China and was first announced on December 31, 2019, have been reported worldwide as of January 19, 2021 [3]. In Korea, from January 20, 2020 (when the first confirmed case was reported) to March 1, 2021, 90,029 COVID-19 patients have been recorded.

Approximately 1 year since COVID-19 first emerged, the world is facing a new stage of the pandemic due to variants. The first infection with variant originating from the United Kingdom (UK) was reported on September 20, 2020 [1], and variants of SARS-CoV-2, the virus that causes COVID-19, have since spread rapidly around the world. In Korea, the first patient infected with the variant originating from the UK was first found at entry screening in December 2020, and 162 patients with COVID-19

variants have been reported since. Increased transmissibility (1.5 times higher) has been reported for the variant originating from the UK [1,4]. The possibility of higher transmissibility has been suggested for the variant originating from the South Africa, Brazil [5,8], as well as the possibility that the variants may evade antibodies depending on the site of variant Spike protein in the virus [6,7]. The situation requires further research.

In order to respond the spread of SARS-CoV-2 variants in Korea, individuals who are entering from high-risk countries with outbreaks of variants of concern (VOCs) are required to submit the result of a PCR negative and go through a strengthened quarantine process after testing [2]. Moreover, an enhanced patient management protocol has been applied to individuals who are diagnosed with COVID-19 after entering from high-risk countries affected by VOCs and to patients who are confirmed to have VOCs. In the enhanced patient management protocol, patients who are suspected or confirmed to have been infected with a VOC are isolated in a separate room and the enhanced case management guidelines is implemented. According to the temporary test-based guideline for quarantine release, individuals with 2 consecutive negative PCR tests are released. However, research on VOCs is ongoing; thus, once scientific evidence on the transmission period of VOCs becomes available, an evidence-based guidance on discharging patients with VOCs will be prepared.

This study aimed to analyze the epidemiological and clinical characteristics of patients with VOC in Korea in order to establish a response strategy and VOCs patient management policy based on regular monitoring.

Methods

This study conducted a frequency analysis and used

the chi-square test to analyze data from initial and in-depth epidemiological investigation results and clinical information from 162 patients infected with the VOCs originating from the UK, South Africa, and Brazil (confirmed in South Korea from December 28, 2020 to March 1, 2021) using R. Epidemiological and clinical characteristics of the 162 patients (138 with the VOCs originating from the UK, 18 with the VOCs originating from the South Africa, and 6 with the VOCs originating from the Brazil) were analyzed.

Results

1. Route of infection and detection

In total, 162 patients infected with the VOCs originating from the UK, South Africa, and Brazil were confirmed in Korea from December 28, 2020 to March 1, 2021. Of these cases, 127 (78.4%) were imported cases, among which cases confirmed during home quarantine were most frequent (n=67, 41.4%), followed by cases confirmed at entry screening (n=58, 35.8%) and cases exempt from quarantine and confirmed with tests after entry (n=2, 2.1%). Thirty-five cases (21.6%) were locally acquired, among whom 32 cases (19.8%) had contact with confirmed cases and the remaining 3 cases (1.9%) were under investigation (Table 1).

2. Epidemiological characteristics

A. 501Y.V1

Most VOCs patients in Korea had the VOCs originating from the UK (138 out of 162, 85.2%). There were more male (n=91, 65.9%) than female (n=47, 34.1%), and most patients

Table 1. Route of infection and detection of VOCs in Korea

	Total	501Y.V1 (originating from the UK)	501Y.V2 (originating from the South Africa)	501Y.V3 (originating from the Brazil)	p-value**
Total	162 (100.0%)	138 (100.0%)	18 (100.0%)	6 (100.0%)	
Imported cases	127 (78.4%)	104 (75.4%)	17 (94.4%)	6 (100.0%)	
At entry screening	58 (35.8%)	48 (34.8%)	8 (44.4%)	2 (33.3%)	
During home quarantine	67 (41.4%)	54 (39.1%)	9 (50.0%)	4 (66.7%)	0.398
Others*	2 (1.2%)	2 (1.4%)	0 (0.0%)	0 (0.0%)	
Locally-acquired cases	35 (21.6%)	34 (24.6%)	1 (5.6%)	0 (0.0%)	
Contact with confirmed cases	32 (19.8%)	31 (22.5%)	1 (5.6%)	0 (0.0%)	
Under investigation (unclassified)	3 (1.9%)	3 (2.2%)	0 (0.0%)	0 (0.0%)	0.270

* Home quarantine exemption; ** χ^2 test

were in their 30s (n=34, 24.6%), followed by those in their 20s (n=28, 20.3%) and 40s (n=26, 18.8%). The majority of patients were isolated in hospitals (n=73, 52.9%), followed by residential treatment centers (n=63, 45.7%) and home (n=1, 0.7%). Thirty-six patients were released from isolation in accordance with the test-based guidance on discharging patients in the enhanced case management guidelines. The average length of isolation was 25.9 days (Table 2).

B. 501Y.V2

Eighteen of the 162 (11.1%) VOC patients in Korea had the VOCs originating from the South Africa . There were more male (n=11, 61.1%) than female (n=7, 38.9%), and most patients were in their 30s (n=6, 33.3%), followed by those in their 20s and 40s (n=4, 22.2%, respectively). Most patients were isolated in residential treatment centers (n=11, 61.1%), followed by hospitals (n=6, 33.3%) and home (n=1, 5.6%). There were no severe/critical cases, including death. Seven patients were released from isolation in accordance with the test-based guidance on discharging patients in the enhanced patient management guidelines. The average length of isolation was 25.9 days,

which was identical to the average for patients with the VOCs originating from the UK (Table 2).

C. 501Y.V3

Six of the 162 (3.7%) VOC patients in Korea had the VOCs originating from the Brazil. There were more male (n=4, 66.7%) than female (n=2, 33.3%), with 2 patients (33.3%) each in their 30s and 60s and 1 patient (16.7%) each in their 20s and 60s. Most patients were isolated in residential treatment centers (n=4, 66.7%), followed by hospitals (n=2, 33.3%). There were no severe/critical cases, including death. Two patients were released from isolation in accordance with the test-based guidance on discharging patients in the enhanced patient management guidelines. The average length of isolation was 22.0 days, which was 3 days shorter than the average of patients with the VOCs originating from the UK, South Africa (Table 2).

3. Clinical characteristics

More than half of the VOC patients in Korea reported symptom (n=100, 61.7%), while 62 patients were asymptomatic

Table 2. Epidemiological characteristics of VOCs in Korea

	Total	501Y.V1 (originating from the UK)	501Y.V2 (originating from the South Africa)	501Y.V3 (originating from the Brazil)	<i>p</i> -value**
Total	162 (100.0%)	138 (85.2%)	18 (11.1%)	6 (3.7%)	
Gender					
Male	106 (65.4%)	91 (65.9%)	11 (61.1%)	4 (66.7%)	0.919
Female	56 (34.6%)	47 (34.1%)	7 (38.9%)	2 (33.3%)	
Nationality					
Koreans	105 (64.8%)	90 (65.2%)	9 (50.0%)	6 (100.0%)	0.082
Foreigners	57 (35.2%)	48 (34.8%)	9 (50.0%)	0 (0.0%)	
Age group (yrs)					
0-9	10 (6.2%)	9 (6.5%)	1 (5.6%)	0 (0.0%)	0.878
10-19	11 (6.8%)	10 (7.2%)	1 (5.6%)	0 (0.0%)	
20-29	33 (20.4%)	28 (20.3%)	4 (22.2%)	1 (16.7%)	
30-39	42 (25.9%)	34 (24.6%)	6 (33.3%)	2 (33.3%)	
40-49	30 (18.5%)	26 (18.8%)	4 (22.2%)	0 (0.0%)	
50-59	18 (11.1%)	17 (12.3%)	0 (0.0%)	1 (16.7%)	
60-69	15 (9.3%)	11 (8.0%)	2 (11.1%)	2 (33.3%)	
70-79	1 (0.6%)	1 (0.7%)	0 (0.0%)	0 (0.0%)	
80+	2 (1.2%)	2 (1.4%)	0 (0.0%)	0 (0.0%)	
Isolation place					
Residential treatment center	78 (48.1%)	63 (45.7%)	11 (61.1%)	4 (66.7%)	0.619
Hospital	81 (50.0%)	73 (52.9%)	6 (33.3%)	2 (33.3%)	
Home treatment	2 (1.2%)	1 (0.7%)	1 (5.6%)	0 (0.0%)	
Others*	1 (0.6%)	1 (0.7%)	0 (0.0%)	0 (0.0%)	

* Death before COVID-19 confirmation; ** χ^2 test

(38.3%). When the reported symptoms were categorized (excluding asymptomatic cases), the most frequent symptom was mild respiratory symptoms without fever (e.g., coughing) (n=37, 22.8%), followed by mild respiratory symptoms with fever (n=27, 16.7%), fever (n=18, 11.1%), other symptoms (e.g., chills, stomachaches) with (n=8, 4.9%) and without fever (n=8, 4.9%), and an acute loss of sense of smell or taste (n=2, 1.2%) (Table 3).

In Korea, patients who are isolated and treated with high-flow oxygen therapy, ventilator, ECMO (extracorporeal membrane oxygen) or CRRT (continuous renal replacement therapy) are classified as severe/critical cases. The main

symptoms reported by VOCs patients in Korea were mostly mild, but 5 patients with the VOCs originating from the UK were classified as severe/critical cases (including 1 death). The proportion of severe/critical cases among VOCs patients in Korea was 3.09%, and the fatality rate was 0.6% (Table 3). Comparing the proportion of severe/critical cases and fatality rate of VOC patients and non-VOC patients, no major difference was observed. However, since research on VOCs is continuing and the number of VOCs patients in Korea is increasing, ongoing monitoring and data analysis are necessary.

Table 3. Clinical characteristics of VOCs in Korea

	Total	501Y.V1 (originating from the UK)	501Y.V2 (originating from the South Africa)	501Y.V3 (originating from the Brazil)	p-value*
Total	162 (100.0%)	138 (85.2%)	18 (11.1%)	6 (3.7%)	
Symptom					
Symptomatic	100 (61.7%)	85 (61.6%)	11 (61.1%)	4 (66.7%)	0.967
Asymptomatic	62 (38.3%)	53 (38.4%)	7 (38.9%)	2 (33.3%)	
Symptom classification					
Fever only	18 (11.1%)	11 (8.0%)	6 (33.3%)	1 (16.7%)	0.027
Fever and respiratory symptoms	27 (16.7%)	27 (19.6%)	0 (0.0%)	0 (0.0%)	
Fever and other symptoms	8 (4.9%)	6 (4.3%)	2 (11.1%)	0 (0.0%)	
Respiratory symptoms without fever	37 (22.8%)	33 (23.9%)	2 (11.1%)	2 (33.3%)	
Acute loss of sense of smell or taste	2 (1.2%)	1 (0.7%)	1 (5.6%)	0 (0.0%)	
Others	8 (4.9%)	7 (5.1%)	0 (0.0%)	1 (16.7%)	
Asymptomatic	62 (38.3%)	53 (38.4%)	7 (38.9%)	2 (33.3%)	
Severity					
Severe/critical	4 (2.5%)	4 (2.9%)	0 (0.0%)	0 (0.0%)	0.924
Mild/asymptomatic	157 (96.9%)	133 (96.4%)	18 (100.0%)	6 (100.0%)	
Death	1 (0.6%)	1 (0.7%)	0 (0.0%)	0 (0.0%)	

* χ^2 test

Conclusion

The past year (2020) has been profoundly shaped by the COVID-19 pandemic, which started in Wuhan, Hubei Province, China and was first reported on December 31, 2019. Infection with a variant of COVID-19 was reported in the United Kingdom on September 20, 2020; since then, COVID-19 variants have spread around the world. A high transmissibility (1.5 times) has been reported for the VOCs originating from the UK [1,4], and the possibility of higher transmissibility has been suggested for the VOCs originating from the South Africa and Brazil [5, 8]. The possibility of antibody evasion depending on the site of variant Spike protein in the virus has been reported [6,7], but

more research is needed. Therefore, it is necessary to continue analyzing epidemiological and clinical information about VOC patients in Korea and to establish a VOCs patient management response strategy.

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Conflict of Interest

No potential conflict of interest relevant to this article was reported.

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① What was known?

Since the first patient with a COVID-19 variant was confirmed in Korea in December 2020, a total of 162 patients with VOCs have been confirmed as of March 1, 2021, with 138 patients having the VOCs originating from the UK, 18 having VOCs originating from the South Africa, and 6 having VOCs originating from the Brazil.

② What does this study add?

Among the 162 patients, there were more male (n=106, 65.4%) than female (n=56, 34.6%). Most patients were in their 30s (n=42, 25.9%), and the average age was 36.4 years. Among the VOCs patients in Korea, 100 (61.7%) were symptomatic, while 62 (38.3%) were asymptomatic. The main symptom reported was mild respiratory symptoms without fever (n=37, 22.8%). 5 severe/critical cases of the VOCs originating from the UK occurred, including 1 death.

③ What are the Implications?

Based on the ongoing monitoring of the clinical status of patients with VOCs, a response strategy for VOC patient management should be established according to the characteristics (severity and fatality) of VOCs.

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Cases of outbreaks caused by COVID-19 variants in the Republic of Korea

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Abstract

In December 2020, the UK variant of concern (VOC) of SARS-CoV-2, the virus that causes COVID-19, was first identified in an international traveler entering South Korea. Thereafter, 162 cases of VOCs occurred and 5 cases of VOCs in cluster outbreaks were confirmed as of March 1, 2021. Detailed epidemiological investigations were conducted for 3 outbreaks. The purpose of this report was to describe the transmission pathways and epidemiological relationships between groups, and to present the results of contact follow-up management. On the basis of this report, it is recommended to respond proactively to the occurrence of confirmed patients in groups with a high risk of having VOCs and to establish measures to prevent spread in the local community.

Keywords: COVID-19, Variant, inflow from abroad

Introduction

The variants of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) reported in the United Kingdom, South Africa, and Brazil between December 2020 and January 2021 are reported to differ from non-mutant forms of SARS-CoV-2 in terms of transmissibility and immune response. Countries throughout the world are strengthening the monitoring and management of SARS-CoV-2 variants [1,2].

In South Korea, in order to minimize imported cases and locally transmitted cases, strengthened measures have been implemented, including expanded virus monitoring for individuals traveling from abroad, stricter quarantine, enhanced infection management within treatment facilities for individuals

confirmed to have a variant of concern (VOC), and an expanded range of contact investigation and testing [3].

The variant originating from the United Kingdom (501Y.V1) was first detected in an individual entering South Korea from abroad in December 2020, and a total of 162 cases have since been confirmed as of March 1, 2021 [4]. As of January 2021, the VOC patients confirmed in South Korea were 5 cohabitating family members of the imported case. A locally transmitted VOC case was confirmed in a local contact outside of the cohabitating family members on February 1, 2021; therefore, to reduce additional local transmissions, the transmission route and contacts were re-investigated, and VOC monitoring was strengthened in the locations where infections occurred in order to understand the extent of the spread.

This report was prepared for use as reference material for epidemiological investigations and responses to future VOC cluster infections.

the absence of any other epidemiologically possible source of infection despite the lack of confirmation through a laboratory analysis.

Study participants and methods

VOC patients are defined as those who were confirmed to have the UK variant (501Y.V1), the South African variant (501Y.V2), or the Brazilian variant (501Y.V3) based on SARS-CoV-2 whole-genome sequencing [1]. The study participants were drawn from 3 clusters of VOC infections that underwent detailed epidemiological investigations among the 5 clusters that had been identified in South Korea as of March 1. Patients were included in the same cluster if there was a history of contact in terms of time and space during the window of transmission of a previously confirmed case based on an epidemiological investigation of the date of symptom onset and activities of each confirmed case [5]. Among patients in a cluster, a confirmed case of VOC refers to a case when a VOC was confirmed through laboratory analysis, and an epidemiologically related case refers to a case with a confirmed history of contact with a confirmed case of VOC in

Results

The epidemiological pattern, transmission routes, and results of strengthened community monitoring of 3 VOC clusters confirmed as of March 1, 2021 were investigated.

1. Epidemiological patterns

The index patient of cluster 1 was a foreign national who entered South Korea from abroad on December 25, 2020 and was confirmed in a test conducted before release from quarantine on January 7, 2021 (Figure 1). A total of 38 patients were recorded until January 29, 2021, including family members who lived in Jeonnam and visited the home of the index patient during the quarantine period. The index patient of cluster 2 was a foreign national who lived in Siheung-si, Gyeonggi-do, and was confirmed on January 29. Contact tracing of this index patient

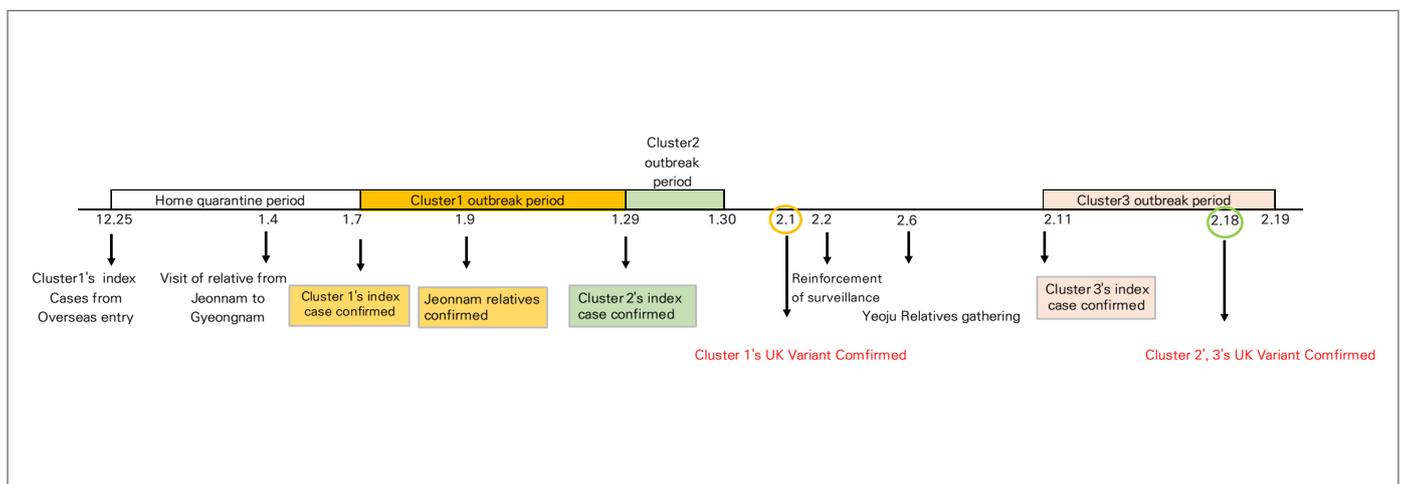


Figure 1. A timeline of the COVID-19 variants group

resulted in 8 cases by January 30. The index patient of cluster 3 was a foreign national residing in Yeosu, Gyeonggi-do, who tested positive on February 10 while living in Jeonnam. By February 23, a total of 31 confirmed cases related to a family gathering on February 6 were reported. As a result of strengthened community monitoring of VOC, the UK variant (501Y.V1) was confirmed on February 18, which was 3 days after the last case in cluster 1, 19 days after the last case in cluster 2, and 8 days after the first case in cluster 3. In all 3 clusters, transmission occurred through family gatherings of foreign residents. Most (over 95%) of the confirmed cases were foreign nationals of a single nationality. In addition to transmission routes within each cluster, transmission routes between clusters were also investigated.

2. Transmission routes

A. Cluster 1 (gathering of foreign relatives in Gyeongnam/Jeonnam)

While the index patient was in quarantine, family members who lived in Jeonnam visited and met with cohabitating family

members of the index patient. After the visit, the visitors and other family members in Jeonnam tested positive. The index patient was a foreign resident and was quarantined at home (second floor of a house) after receiving a negative polymerase chain reaction test conducted at entry. The patient reported that there was no direct contact with family members, but the indoor space was not separated, and exposure between family members was suspected, since the cohabiting and visiting family members tested positive. The VOC-confirmed foreign patients in Gyeongnam/Jeonnam did not have a history of traveling since December and worked in the automobile parts and scrap vehicle export industry. Among 38 cases related to the gathering of the relatives of the foreign resident in Gyeongnam/Jeonnam, 13 were confirmed cases of VOC, and 25 were epidemiologically related cases (Table 1).

B. Cluster 2 (family members in Siheung-si, Gyeonggi-do)

The index patient was a foreign national residing in Siheung-si, Gyeonggi-do, who tested positive on January 29, 2021 (Figure 1). Through contact tracing, 7 family members additionally tested positive, resulting in 8 cases. The patients in this cluster were of

Table 1. Status of variants identification among clusters (as of March 21, 2021)

	Case name	Outbreak period (confirmed date)	Status			Putative infection Route
			Total (foreigner)	Confirmed cases ¹⁾	Epidemiological related cases ²⁾	
Cluster1	Gyeongnam/Jeonnam Foreign Relatives gathering	1.7-1.29.	38 (38)	13 (UK Variant [501Y.V1])	25	Overseas inflow
Cluster2	Family related to Siheung-si, Gyeonggi-do	1.29-1.30.	8 (8)	7 (UK Variant [501Y.V1])	1	Foreign community related
Cluster3	Related to Relatives gathering 2 in Yeosu, Gyeonggi-do	2.10-2.23.	31 (31)	7 (UK Variant [501Y.V1])	24	Foreign community related

1) Variant confirmed cases: A case of confirmed mutant strains (UK, South Africa, Brazil) as a result of the virus analysis

2) Epidemiological related cases: The mutant virus analysis was not performed, but the contact history with the mutant virus infected person was confirmed in a situation where no other infectious source was identified epidemiologically.

the same nationality as the patients in cluster 1 (relatives of the foreign resident in Gyeongnam/Jeonnam) and were in the same industry and community, but no direct connections were made. Global positioning system (GPS) data indicated no extraordinary activities outside of work and home during the contact tracing time period, and none of the 8 cases had any records of travel abroad.

C. Cluster 3 (gathering of relatives in Yeosu, Gyeonggi-do)

Contact tracing following the positive test of the index patient resulted in information about a gathering of relatives in Yeosu on February 6, 2021. Participants in the gathering and related family members also tested positive (Figure 2). The relatives in Jeonnam with whom the index patient was living at the time of testing positive were the index patient's aunt's family. All 8 cohabiting family members tested positive during tracing. The aunt's family members were not contacts of the Gyeongnam/Jeonnam cluster (cluster 1), and they tested negative when all foreign nationals were preemptively tested following identification of the UK variant (501Y1.V1) on February 1, 2021.

The epidemiological investigation showed that the cases in this cluster did not have a history of travel abroad, but were of the same nationality as the previous 2 clusters and were working in the same industry. A total of 31 cases occurred, of which 7 were confirmed VOC cases and 24 were epidemiologically related cases (Table 1).

3. Results of strengthened community monitoring

When a VOC was first confirmed in the cluster involving a gathering of foreign relatives in Gyeongnam/Jeonnam on February 1, diagnostic testing expanded to additionally confirmed contacts and possible contacts identified after re-evaluating the contact management situation. Contacts were assigned to self-isolation, active monitoring, and passive monitoring depending on the level of contact and were tested additionally. Additional testing was given to all cases regardless of the test done before release from quarantine and the presence of symptoms. Possible contacts were also preemptively tested regardless of the presence

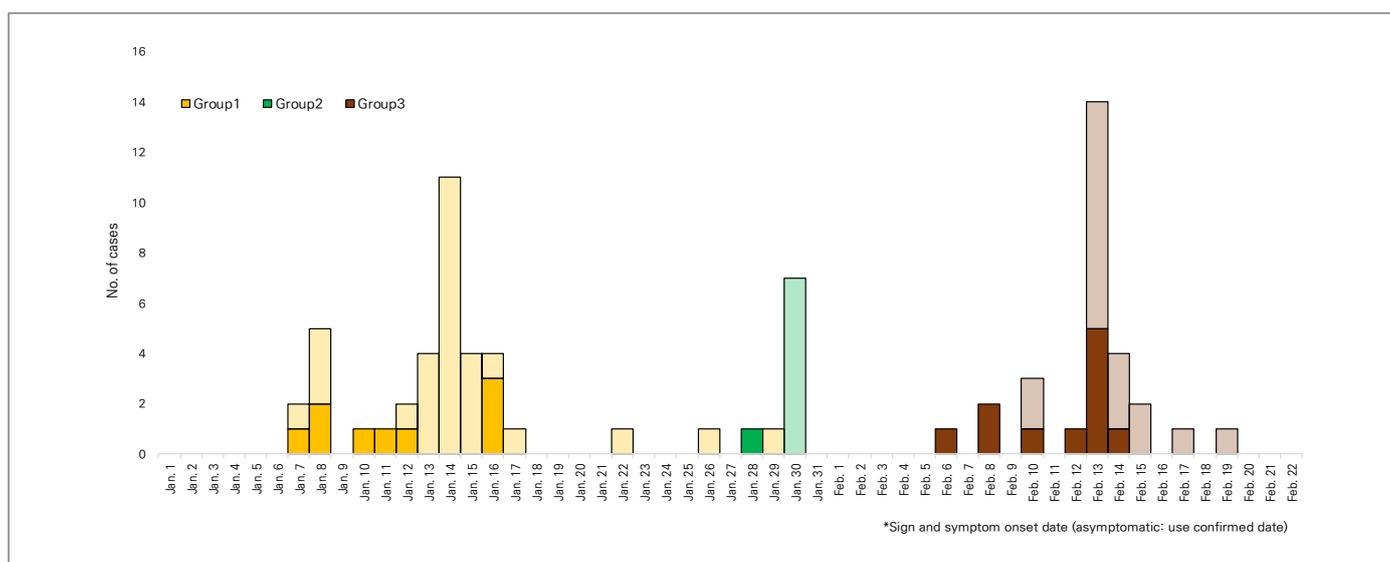


Figure 2. Epidemic curve of the outbreak

Table 2. Results of strengthening community monitoring

Target group		Test (RT-PCR)	Negative	Positive
Management group	Quarantine	52	52	0
	Active monitoring	53	53	0
	Passive monitoring	14	14	0
Preemptive test group	Workplace	383	383	0
	Others (foreigner preemptive test)	128	127	1
	Total	630	629	1

of symptoms. As a result, 630 individuals related to the 3 clusters were tested. Among these individuals, 1 additional case related to the gathering of foreign relatives in Gyeongnam/Jeonnam was identified, but an epidemiological connection to a confirmed case in cluster 1 was not made (Table 2).

Conclusion

VOC clusters occurred in Gimhae, Gyeongnam and Naju, Jeonnam in mid-January, Siheung, Gyeonggi-do in late January, and Yeosu, Gyeonggi-do and Naju, Jeonnam after mid-February. All clusters consisted of foreign nationals, and transmission occurred mainly through relatives and family gatherings.

The transmission of cluster 1 is suspected to have originated from an imported case, but patient 0 of the other 2 clusters was not identified. The patients in each cluster reported that the patients in other clusters were not their relatives or acquaintances, but most (over 95%) were foreign nationals of the same nationality, some cases in clusters 1 and 2 lived in the same area, and some cases in clusters 2 and 3 were in the same community within Gyeonggi Province; therefore, it is possible that transmission occurred within this community of foreign nationals.

Strengthened community monitoring found no additional cases other than close contacts of known cases, suggesting that the infection was not widespread in each location. However, the finding of an additional case in a foreign national who did not have an identified contact with known cases suggests that the virus could have been spreading through a different transmission route.

There were some issues in communication when conducting the epidemiological investigation with the foreign nationals, and it was difficult to check movements through GPS as not everyone carried mobile phones at all times. As such, there were various limitations to the information collection during the in-depth investigation. When cases occur among foreign nationals, information should be collected with support from translators or by administering the epidemiological survey in multiple languages. Moreover, it is necessary to further strengthen community monitoring of VOCs and to conduct rapid VOC testing in clusters among foreign nationals.

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Conflict of Interest

No potential conflicts of interest were disclosed.

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① What was previously known?

The variants of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) reported in the United Kingdom, South Africa, and Brazil between December 2020 and January 2021 are reported to differ from non-mutant forms of SARS-CoV-2 in terms of transmissibility and immune response. Countries throughout the world are strengthening the monitoring and management of SARS-CoV-2 variants.

② What is newly learned?

Since the UK variant (501Y.V1) was first detected in an individual entering South Korea from abroad in December 2020, a total of 162 cases of variants of concern (VOCs) were confirmed as of March 1, 2021. Five clusters of VOCs were confirmed as of March 1, 2021. Of these, detailed epidemiological investigations were conducted for 3 clusters. Clusters of 8 to 39 people of family members and relatives of foreign nationals residing in Gyeongnam, Jeonnam, and Gyeonggi-do were identified. An epidemiological connection between the three clusters was not confirmed. Through the strengthened community monitoring conducted after the identification of the VOC infections, 630 additional individuals beyond the initially investigated cases were traced, among whom 1 confirmed VOC case was identified.

③ Implications?

In light of reports that VOCs have higher transmissibility and are associated with a lower efficacy of vaccination, in order to effectively limit the COVID-19 pandemic moving forward, expanded monitoring of VOCs and strengthened patient and contact tracing and management should continue.

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우리나라 만성폐쇄성폐질환의 유병 및 관리 현황

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초 록

전 세계적으로 약 320만여 명이 만성폐쇄성폐질환으로 사망하여 전체 사망의 5%를 차지하고 있고, 전 세계 인구의 약 12%가 만성폐쇄성폐질환을 앓고 있다. 만성폐쇄성폐질환의 가장 중요한 위험 요인은 흡연으로 만성폐쇄성폐질환으로 인한 사망의 약 80%가 흡연에 기인한다고 할 수 있다. 본 보고서에서는 우리나라의 만성폐쇄성폐질환의 유병 및 관리 현황을 살펴보고, 향후 정책수립의 기초자료를 제시하고자 하였다.

우리나라에서 만성폐쇄성폐질환의 유병률은 매년 감소하는 추세를 보이다가 2019년에 다시 증가하여 10.8%이었다. 40대 3.1%, 50대 8.7%, 60대 19.1%, 70세 이상 27.3%로 연령이 증가할수록 만성폐쇄성폐질환의 유병률이 증가하였다. 여자의 경우는 40대 2.2%, 50대 3.7%, 60대 9.0%, 70세 이상 17.4%이었고, 남자의 경우는 40대 3.9%, 50대 13.7%, 60대 31.2%, 70세 이상 39.9%이었다. 2019년 남자의 유병률(16.3%)이 여자(5.9%)에 비해 2.8배 높았으며, 지난 2007년에서 2019년까지의 유병률 감소는 남자(28%)보다 여자(37%)에게서 더 두드러졌다. 또한 우리나라의 만성폐쇄성폐질환 유병자 중 이전에 의사로부터 진단을 받은 경우는 2.5%로 고혈압(71.4%), 당뇨병(65.2%), 고콜레스테롤혈증(61.7%)에 비해서 월등히 낮았으나, 치료율은 만성폐쇄성폐질환(84.5%)이 고혈압(67.1%), 당뇨병(60.8%), 고콜레스테롤혈증(53.1%)보다 높았다. 우리나라에서는 만성폐쇄성폐질환 관리를 위해 2013년부터 매년 영양급여 적정성 평가를 실시해 오고 있으며, 일차의료기관용 진료지침과 일반국민용 교육자료 배포 등을 통해 조기발견 노력을 기울이고는 있으나 종합적인 관리는 미흡한 실정이다.

이상의 결과를 통해 볼 때, 우리나라에서 만성폐쇄성폐질환 관리는 조기진단에 집중할 필요가 있다 하겠다. 특히, 40세 이상의 남자 흡연자를 대상으로 한 금연과 조기발견 프로그램이 우선적으로 고려될 필요가 있다.

주요 검색어 : 만성폐쇄성폐질환, 유병률, 의사진단율, 조기발견율, 흡연

들어가는 말

만성호흡기질환(chronic respiratory diseases, CRDs)은 기도(airways)와 폐의 구조(structures)에 발생하는 질병으로, 대표적인 질병으로는 만성폐쇄성폐질환(chronic obstructive pulmonary disease, COPD)과 천식(asthma)이 있다[1]. 천식은 만성폐쇄성폐질환에 비해 유병률이 2배 정도 높아서 전 세계에서 가장 유병률이 높은 만성호흡기질환이나,

사망률로 보면 만성폐쇄성폐질환의 사망률이 천식에 비해 8배나 높다[2]. 2015년 기준으로 전 세계에서 약 320만 명¹⁾이 만성폐쇄성폐질환으로 사망하여 전 세계 사망의 약 5%를 차지하였으며[1,3], 이러한 사망자의 90% 이상이 저소득 및 중위소득 국가에서 발생하고 있다[1,3,4]. 만성폐쇄성폐질환의 전 세계 유병률은 약 12% 수준이며[5], 전 세계 30세 이상의 연령에서 만성폐쇄성폐질환으로 의사진단을 받은 경우는 2015년에 약 2.5억 명에서 3.8억 명에 달한다[2,5,6]. 한편, 2015년 기준으로 전 세계

1) 2015년에 전 세계에서 천식으로 인한 사망은 49만5천 명 수준이다.

장애보정손실연수(disability-adjusted life year, DALYs)의 1.1%가 천식이 차지한 반면, 2.6%가 만성폐쇄성폐질환에 기인한 것으로 분석되었다[2]. 이처럼 만성폐쇄성폐질환은 질병부담이 큰 만성질환 중 하나이므로, 본 보고서에서는 우리나라의 만성폐쇄성폐질환의 사망과 유병 현황을 살펴보고, 만성폐쇄성폐질환의 의사진단율과 치료를 등의 관리 현황과 정책을 살펴봄으로써 향후 우리나라의 관련 정책 수립에 필요한 기초 자료를 제공하고자 하였다.

몸 말

1. 사망 현황

우리나라에서는 2019년 기준으로 연간 6천 2백여 명이 만성하 기도질환²⁾으로 사망하여 전체 사망의 2.1%를 차지하였고, 인구 10만

명당 사망률은 12.0명³⁾으로 사망원인 9위를 차지하였다(표 1). 이는 지난 1989년에 만성하기도질환으로 인한 사망률이 인구 10만 명당 9.1명(1.6%, 8위)에서 1999년 및 2009년에 각각 13.7명(2.6%, 8위) 및 13.9명(2.8%, 7위)으로 증가하다가 다소 감소한 수준이다[7].

세계보건기구(World Health Organization, WHO)가 발표한 바에 따라 주요국의 만성호흡기질환으로 인한 사망을 살펴보면 다음과 같다(표 2). 전 세계 사망 중 만성질환으로 인한 사망은 71%이고, 전체 사망 중 만성호흡기질환으로 인한 사망은 5%를 차지하여 만성질환으로 인한 사망 중 만성호흡기질환의 사망은 7%를 차지하였다. 우리나라는 전체 사망 중 만성호흡기질환으로 인한 사망이 6%로 미국(9%)과 일본(9%)보다는 다소 낮았고 독일(6%)과는 비슷한 수준이었다. 또한 우리나라의 만성질환 사망 중 만성호흡기질환의 사망 비중은 7.5%로 전 세계 평균(7.0%), 독일(6.7%) 및 우간다(6.1%)보다는 다소 높았고, 미국(10.2%) 및 일본(11.3%)보다는 낮은 수준이었다[8].

표 1. 우리나라 만성하기도질환 사망률의 변화

단위: %, 명/10만 명

1989년			1999년			2009년			2019년		
사망순위	%	사망률	사망순위	%	사망률	사망순위	%	사망률	사망순위	%	사망률
8위	1.6	9.1	8위	2.6	13.7	7위	2.8	13.9	9위	2.1	12.0

자료: 통계청. 사망 원인 통계. 각 연도.

표 2. 국가별 만성호흡기질환으로 인한 사망 비율

단위: %

구분	전 세계 ^{1,2,3)}	한국	일본	미국	독일	우간다
만성질환 전체	71	80	82	88	91	33
- 만성호흡기질환	5 (7.0)	6 (7.5)	9 (11.3)	9 (10.2)	6 (6.7)	2 (6.1)
만성질환 이외의 질환	29	20	18	12	9	67
합계	100	100	100	100	100	100

주: () 은 만성질환으로 인한 사망 중 만성호흡기질환의 사망이 차지하는 비중

자료: 1) World Health Organization. Chronic Respiratory Disease. *Health Topics*. <https://www.who.int/health-topics/chronic-respiratory-diseases>.

2) World Health Organization. Chronic Obstructive Pulmonary Disease (COPD). *Factsheet*. 1 December, 2017.

3) World Health Organization. Noncommunicable diseases country profiles. 2018.

2) 만성하기도질환은 허혈성 심장 질환, 뇌졸중에 이어 세계 사망 원인 3위를 차지하고 있다. 2015년 기준으로 전 세계에서 약 3.2백 만 명이 만성폐쇄성폐질환으로 사망(전 세계 사망의 5%)하였다[1,3].

3) 전 세계 만성하기도질환의 사망률은 2015년 기준으로 인구10만 명당 41명이다[2].

2. 유병 현황

전 세계의 만성폐쇄성폐질환의 유병률은 12.2%이며 남자 15.7%, 여자 9.9%로 남자에게서 더 빈번하였고, 연령별로는 50세 이하 5.3%, 50~59세 10.2%, 60세 이상 21.4%로 연령이 증가할수록 높았다(표 3). 흡연여부에 따라서는 현재 흡연자가 18.4%로 가장 높았고, 과거 흡연자 16.3%, 비흡연자는 7.2%로 흡연경험에 따라 유병률의 차이가 있었다[7].

1990년부터 2010년까지 20년간의 유병률의 변화를 살펴보면, 1990년에 10.7%이었던 유병률이 2010년 11.7%로 지난 20년간 1.0%포인트(9.3%) 증가하였다(표 3). 이를 지역별로 살펴보면

동남아시아 지역이 가장 많이 증가하였고(22.8%), 서태평양 지역(20.7%), 아프리카 지역(16.3%), 유럽 지역(16.1%), 아메리카 지역(14.3%), 중동 지역(13.6%) 순이었다. 2010년의 도시와 농촌 간 만성폐쇄성폐질환의 유병률은 각각 13.6%와 9.7%로 지난 20년 전에 비해 그 증가율이 각각 3.0% 및 10.2%로 농촌에서의 만성폐쇄성폐질환 유병률⁴⁾ 증가 폭이 컸다[4].

우리나라에서 만 40세 이상의 만성폐쇄성폐질환 유병률은 매년 조금씩 낮아지고 있는 추세이나 2019년에는 다소 증가하였다[9]. 2019년의 유병률은 11.8%이었으며, 여자(5.9%)보다 남자(16.3%)에게서 더욱 빈번⁵⁾하였다(그림 1). 이를 연령별로 살펴보면, 여자의 경우, 40~49세 2.2%, 50~59세 3.7%, 60~69세

표 3. 전 세계 만성폐쇄성폐질환 유병률

구분		추계 ¹⁾	1990 ²⁾	2010 ²⁾	변화(율)
전 세계		12.2	10.7	11.7	1.0%p (9.3)
성별	남자	15.7	n.a.	n.a.	n.a.
	여자	9.9	n.a.	n.a.	n.a.
연령	50세 이하	5.3	n.a.	n.a.	n.a.
	50~59세	10.2	n.a.	n.a.	n.a.
	60세 이상	21.4	n.a.	n.a.	n.a.
흡연여부	현재흡연자	18.4	n.a.	n.a.	n.a.
	과거흡연자	16.3	n.a.	n.a.	n.a.
	비흡연자	7.2	n.a.	n.a.	n.a.
도농 구분	도시	n.a.	13.2	13.6	0.4%p (3.0)
	농촌	n.a.	8.8	9.7	0.9%p (10.2)
WHO지역	아프리카(AFRO)	n.a.	9.8	11.4	1.6%p (16.3)
	아메리카(AMRO)	n.a.	13.3	15.2	1.9%p (14.3)
	중동(EMRO)	n.a.	11.8	13.4	1.6%p (13.6)
	유럽(EURO)	n.a.	11.8	13.7	1.9%p (16.1)
	동남아시아(SEARO)	n.a.	7.9	9.7	1.8%p (22.8)
	서태평양(WPRO)	n.a.	9.2	11.1	1.9%p (20.7)

주: * 전체 인구 대상 유병률, ** 만 30세 이상

자료: 1) Varmaghani M., Dehghani M., Heidari E., Sharifi F., Moghaddam S., Farzadfar F. Global prevalence of chronic obstructive pulmonary disease: systematic review and meta-analysis. *East Mediterr Health J*, 2019; 25(1):47-57.

2) Adeloje D., Chua S. Lee C., Basquill C., Papan A., Theodoratou E et al., Global and Regional Estimates of COPD Prevalence: Systematic Review and Meta-analysis. *Journal of Global Health*, 2015;5(2):020415. doi: 10.7189/jogh.05-020415.

4) 1990년에서 2015년까지 지난 25년간 만성폐쇄성폐질환의 연령표준화 유병률은 14.7% 감소하였지만, 인구고령화에 따라 전 연령에서의 유병률은 44.2%나 증가하였다. 한편, 만성폐쇄성폐질환의 연령표준화 사망률은 지난 25년간 41.9%가 감소하였음에도 불구하고, 인구고령화 및 인구증가에 따라 모든 연령에서의 만성폐쇄성폐질환의 사망자는 11.6% 증가하였다[2].

5) 남자의 만성폐쇄성폐질환 유병률이 여자에 비해 2.8배 높았으며, 지난 2007년에서 2019년까지 여자의 만성폐쇄성폐질환 유병률은 약 37% 감소한 반면, 남자는 28% 감소하여 여자의 유병률 감소 폭이 더 컸다.

9.0%, 70세 이상 17.4%로 연령이 증가할수록 유병률이 증가하였다. 남자의 경우도 40~49세 3.9%, 50~59세 13.7%, 60~69세 31.2%, 70세 이상 39.9%로 연령이 증가할수록 유병률이 증가하였다(그림 2). 한편, 만성폐쇄성폐질환의 연간 진료 인원⁶⁾은 2011년 25.9만여 명에서 2015년 23.2만여 명으로 다소 감소하였다[10].

3. 인지율 및 치료율

만성폐쇄성폐질환의 유병률은 10.8%로 고혈압(28.3%), 당뇨병(11.8%) 및 고콜레스테롤혈증(21.4%)에 비해 낮았으나, 만성폐쇄성폐질환 유병자 중 의사로부터 진단을 받은 경우는 2.5%에 불과하여 고혈압 71.4%, 당뇨병 65.2%, 고콜레스테롤혈증 61.7%에 비해서 월등히 낮았다. 반면, 만성폐쇄성폐질환의 치료율은 84.7%로 고혈압(67.1%), 당뇨병(60.8%), 고콜레스테롤혈증(53.1%)에 비해 높은 수준이었다(표 4).

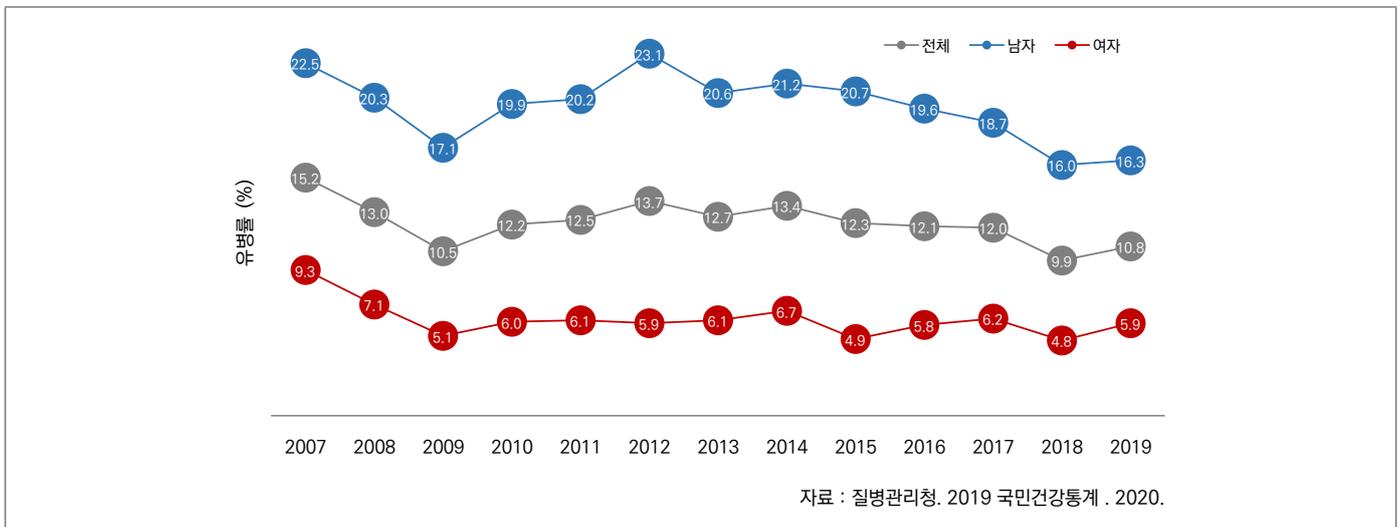


그림 1. 2007~2019 만성폐쇄성폐질환 유병률 추이(만 40세 이상)

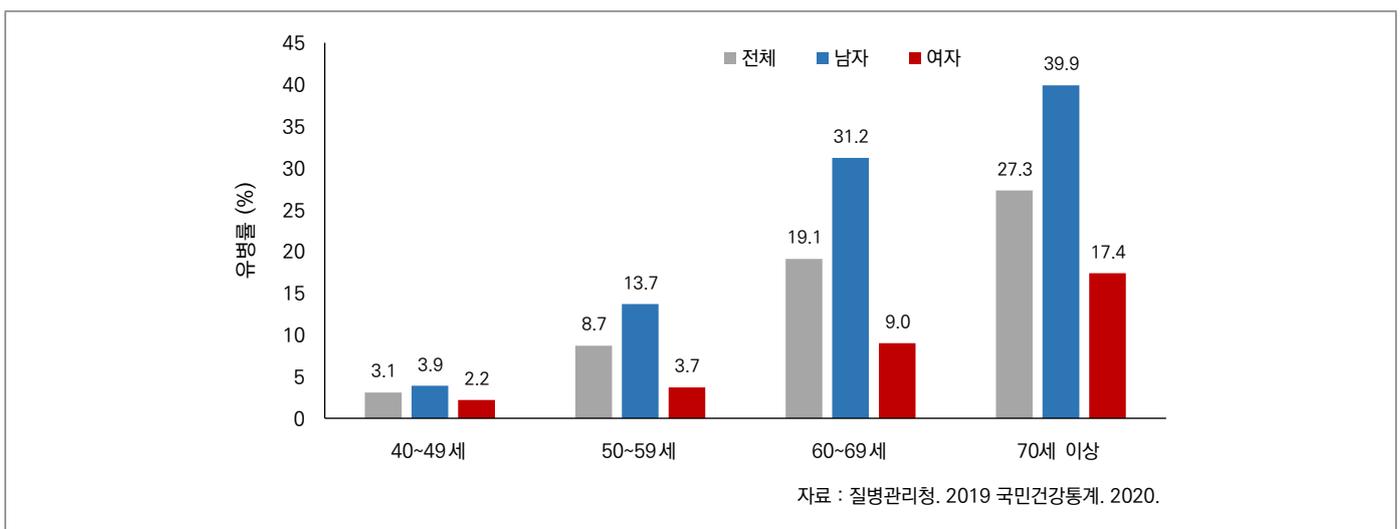


그림 2. 2019년 성별에 따른 연령별 만성폐쇄성폐질환 유병률

6) 천식의 연간 진료 인원은 2013년 179만 명에서 2014년 177만 명, 2015년 165만 명, 2016년 163만 명, 2017년 142만 명으로 감소하는 추세를 보였다[11].

표 4. 주요 만성질환과 만성폐쇄성폐질환의 관리수준 비교

단위: %

주요 만성질환	유병률			인지율			치료율		
	2009	2015	2019	2007~2009	2013~2015	2019	2007~2009	2013~2015	2019
고혈압	26.3	27.8	27.2	66.3	67.3	71.4	60.3	63.6	67.1
당뇨병	11.6*	10.2	11.8	-	61.0	65.2	-	54.8	60.8
고콜레스테롤혈증	11.4	17.9	22.3	38.8	57.7	61.7	26.9	45.5	53.1
만성폐쇄성폐질환	10.5	12.3	10.8	-	-	2.5 [†]	-	85.5 [‡]	84.5 [§]

주: 만 30세 이상 통계[(만성폐쇄성폐질환은 만40세 이상) : 인지율(유병자 중 의사진단을 받은 경우), 치료율(유병자 중 치료자)]

* 2011년 통계, † 2016-2018년 통합자료(40세이상), ‡ 2014년 심평원 적정성 평가결과의 지속방문 환자비율, § 2018년 심평원 적정성 평가결과의 지속방문 환자비율 [11]

자료: 1) 질병관리청, 2019 국민건강통계, 2020.

2) 건강보험심사평가원, 보도자료: 천식(제6차) 및 만성폐쇄성폐질환(제5차) 적정성 평가 결과, 2020.5.28.

4. 관련 정책 현황

우리나라는 천식과 만성폐쇄성폐질환을 관리하기 위하여 각각 2012년과 2013년에 요양급여 적정성 평가를 도입하였다. 천식의 경우는 2012년에 도입하여 2013년도 1차 평가를 실시하여 온 이래 2018년 6차 평가까지 실시하였고, 만성폐쇄성폐질환의 경우는 2014년에 1차 평가를 실시하여 2018년까지 5차에 걸친 평가를 실시한 바 있다. 2018년 평가 결과를 살펴보면, 폐기능검사 시행률은 천식 35.1%, 만성폐쇄성폐질환 73.5%였으며, 이는 각각 2014년의 24.9% 및 58.7%보다 증가하였다. 그리고 천식환자에 대한 흡입스테로이드 처방환자 비율은 2014년 27.1%에서 2018년 39.0%로 증가하였고, 만성폐쇄성폐질환환자에 대한 흡입기관지확장제 처방환자 비율 역시 2014년 67.9%에서 2018년 83.0%로 증가하였다. 다만, 지속방문환자 비율의 경우는 2018년 천식 및 만성폐쇄성폐질환이 각각 73.2% 및 84.5%로 지난 2014년의 71.9% 및 85.5%에 비해 개선되지는 않았다[12].

질병관리청에서는 2007년부터 국민건강영양조사에서 만성폐쇄성폐질환의 유병률을 산출해 오고 있으며[9], 일차 의료기관에서 사용할 수 있는 만성폐쇄성폐질환 진료지침과 일반국민이 사용할 수 있는 교육자료를 마련하여 배포⁷⁾ 한 바 있다. 그리고 국가건강정보포털(<https://health.cdc.go.kr>)에서도

만성폐쇄성폐질환에 관한 건강정보와 동영상 자료 등을 게시하고 있다. 그러나 만성폐쇄성폐질환에 관한 종합적인 관리는 아직 미흡하다 하겠다[13].

맺는 말

만성폐쇄성폐질환은 완치가 가능하지는 않다. 그러나 조기에 발견하여 치료를 하면 증상을 완화시킬 수 있고 사망의 위험을 줄여줄 수 있으며, 삶의 질 역시 향상시킬 수 있다[1]. 만성폐쇄성폐질환의 주요 위험요인으로는 흡연, 간접흡연, 실내공기오염, 실외공기오염, 작업장 먼지 및 화학물질, 아동기의 잦은 하기도감염 등이나, 가장 중요한 위험요인은 흡연이다. 만성폐쇄성폐질환으로 인한 사망의 80%가 흡연에 기인하고 비흡연자보다 흡연자의 만성폐쇄성폐질환으로 인한 사망 가능성이 12~13배 증가하는 점을 고려한다면[14], 흡연자에게 있어 가장 비용 효과적인 치료 방법은 금연이라 하겠다[1,3,5].

우리나라에서 만성폐쇄성폐질환 유병자 중 의사 진단을 받은 경우는 2.5%에 불과하여 우리나라에서의 조기발견 프로그램의 중요성을 보여주었다(표 4). 일차의료기관을 방문하는 만성폐쇄성폐질환자에 대한 조기진단이 중요함에

7) 일차의료용 근거기반 만성폐쇄성폐질환 권고(대한의학회·질병관리본부, 2019년 6월), 나와 가족을 위한 만성폐쇄성폐질환 예방과 관리 정보(대한의학회·질병관리청, 2020년 12월) 등이다.

따라 정부에서는 일차의료기관용 진료지침을 만들어 배포한 바 있지만, 일차의료기관의 적극적인 참여를 위해 보다 다양한 전략이 필요하다. 또한 우리나라의 남자 흡연율이 높고 남자의 만성폐쇄성폐질환 유병률이 높은 점, 그리고 연령이 증가함에 따라 만성폐쇄성폐질환의 유병률이 높아지는 점 등을 고려하여 40세 이상 남자 흡연자를 핵심 정책 대상으로 하여 이들에 대한 금연과 조기진단 프로그램을 우선적으로 마련할 필요가 있다 하겠다.

① 이전에 알려진 내용은?

2015년 기준으로 전 세계에서 약 3.2백만 명이 만성폐쇄성폐질환으로 사망하여 전 세계 사망의 약 5%를 차지하였으며, 만성폐쇄성폐질환의 전 세계 유병률은 약 12% 수준으로 우리나라와 큰 차이는 없었다. 만성폐쇄성폐질환의 가장 중요한 위험 요인은 흡연으로 만성폐쇄성폐질환으로 인한 사망의 약 80%가 흡연에 기인한다고 할 수 있다.

② 새로이 알게 된 내용은?

우리나라에서 만성폐쇄성폐질환의 유병률은 매년 감소하는 추세를 보이다가 2019년에 다시 증가하였다. 2019년 남자의 유병률(16.3%)이 여자(5.9%)에 비해 2.8배 높았으며, 지난 2007년에서 2019년까지의 유병률 감소는 남자(28%)보다 여자(37%)에서 더 두드러졌다. 또한 우리나라의 만성폐쇄성폐질환 유병자 중 의사로부터 진단을 받은 경우는 2.5%에 불과하여 고혈압(71.4%), 당뇨병(65.2%), 고콜레스테롤혈증(61.7%)에 비해서는 월등히 낮았으나, 질병의 치료율은 만성폐쇄성폐질환(84.5%)이 고혈압(67.1%), 당뇨병(60.8%), 고콜레스테롤혈증(53.1%)보다 높게 나타났다.

③ 시사점은?

우리나라의 만성폐쇄성폐질환 유병자 중 의사로부터 진단을 받은 경우는 2.5%에 불과하여, 조기진단의 중요성을 보여주었다. 만성폐쇄성폐질환에 있어서 흡연은 가장 중요한 위험요인이고, 남성일수록, 연령이 높을수록 유병률이 증가하므로, 40세 이상의 남자 흡연자를 대상으로 한 금연과 조기진단 프로그램이 우선적으로 고려될 필요가 있겠다.

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Abstract

Current Status of Chronic Obstructive Pulmonary Disease (COPD) in the Republic of Korea

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According to the World Health Organization (WHO), Chronic Obstructive Pulmonary Disease (COPD) kills approximately 3.2 million people a year worldwide and accounts for approximately 5% of all deaths. The global prevalence of COPD is approximately 12%. Smoking is a leading cause of COPD deaths and nearly 8 out of 10 COPD deaths are a result of smoking. The purpose of this study was to investigate the status of COPD with the aim of identifying mortality, prevalence, and management strategies in the Republic of Korea (ROK). This study analyzed data from Statistics Korea, the Korea Disease Control and Prevention Agency's (KDCA) national health statistics, Korea's Health Insurance Review and Assessment Service (HIRA) and the World Health Organization (WHO). Findings indicated that, in 2019, the prevalence of COPD was 10.8% and the rate among men (16.3%) was higher than that of women (5.9%). The prevalence of COPD declined steadily from 2007 to 2019 and the rate of decrease was 28% among men, compared to 37% among women. The rate of previously diagnosed cases among COPD cases was extremely low (2.5%), compared to other non-communicable diseases (NCDs) such as high blood pressure (71.4%), diabetes (65.2%) and hypercholesterolemia (61.7%). However, the proportion of treatment among people with COPD (84.5%) was higher than that of people with high blood pressure (67.1%), diabetes (60.8%) and hypercholesterolemia (53.1%). This study suggested that policy makers focus their efforts on strategies for early diagnosis of COPD, such as smoking cessation and early detection for men's smokers aged 40 years and over in the ROK.

Keywords: Chronic Obstructive Pulmonary Disease, COPD, Prevalence, Undiagnosed COPD, Detection rate, Smoking

Table 1. Mortality rate of chronic obstructive pulmonary disease (COPD) in the Republic of Korea (ROK)

Unit: %, per 100,000 population

1989			1999			2009			2019		
Rank	%	Mortality									
8th	1.6	9.1	8th	2.6	13.7	7th	2.8	13.9	9th	2.1	12.0

Source: Statistics Korea. Cause of death, 2019.

Table 2. Proportional mortality rate of chronic respiratory diseases (CRDs)

							Unit: %
Category	World ^{1,2,3)}	Korea	Japan	USA	Germany	Uganda	
Non-communicable diseases (NCDs)	71	80	82	88	91	33	
- Chronic respiratory diseases (CRDs)	5 (7.0)	6 (7.5)	9 (11.3)	9 (10.2)	6 (6.7)	2 (6.1)	
Other Diseases	29	20	18	12	9	67	
Total	100	100	100	100	100	100	

Note: () is the proportion of deaths induced CRDs among NCDs

Source: 1) World Health Organization, Chronic Respiratory Disease, Health Topics,

<https://www.who.int/health-topics/chronic-respiratory-diseases>.

2) World Health Organization, Chronic Obstructive Pulmonary Disease (COPD), *Factsheet*, 1 December, 2017.

3) World Health Organization, Noncommunicable diseases country profiles, 2018.

Table 3. Global prevalence of chronic obstructive pulmonary disease (COPD)

					Unit: %
Category	Estimated ¹⁾	1990 ^{**2)}	2010 ^{**2)}	Changes from 1990 to 2010	
World	12.2	10.7	11.7	1.0%p (9.3)	
Gender					
Men	15.7	n.a.	n.a.	n.a.	
Women	9.9	n.a.	n.a.	n.a.	
Age groups, yr					
< 50	5.3	n.a.	n.a.	n.a.	
50~59	10.2	n.a.	n.a.	n.a.	
≥ 60	21.4	n.a.	n.a.	n.a.	
Smoking status					
Current smokers	18.4	n.a.	n.a.	n.a.	
Ex-smokers	16.3	n.a.	n.a.	n.a.	
Never smokers	7.2	n.a.	n.a.	n.a.	
Area					
Urban	n.a.	13.2	13.6	0.4%p (3.0)	
Rural	n.a.	8.8	9.7	0.9%p (10.2)	
WHO Regions					
Africa (AFRO)	n.a.	9.8	11.4	1.6%p (16.3)	
Americas (AMRO)	n.a.	13.3	15.2	1.9%p (14.3)	
Eastern Mediterranean (EMRO)	n.a.	11.8	13.4	1.6%p (13.6)	
Europe (EURO)	n.a.	11.8	13.7	1.9%p (16.1)	
South-East Asia (SEARO)	n.a.	7.9	9.7	1.8%p (22.8)	
Western Pacific (WPRO)	n.a.	9.2	11.1	1.9%p (20.7)	

Note: *general population, **people aged 30 years or over

Source: 1) Varmaghani M., Dehghani M., Heidari E., Sharifi F., Moghaddam S., Farzadfar F. Global prevalence of chronic obstructive pulmonary disease: systematic review and meta-analysis. *East Mediterr Health J*, 2019; 25(1):47-57.

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Table 4. Prevalence, diagnosis, and treatment among chronic obstructive pulmonary disease (COPD) and other non-communicable diseases (NCDs)

Unit: %

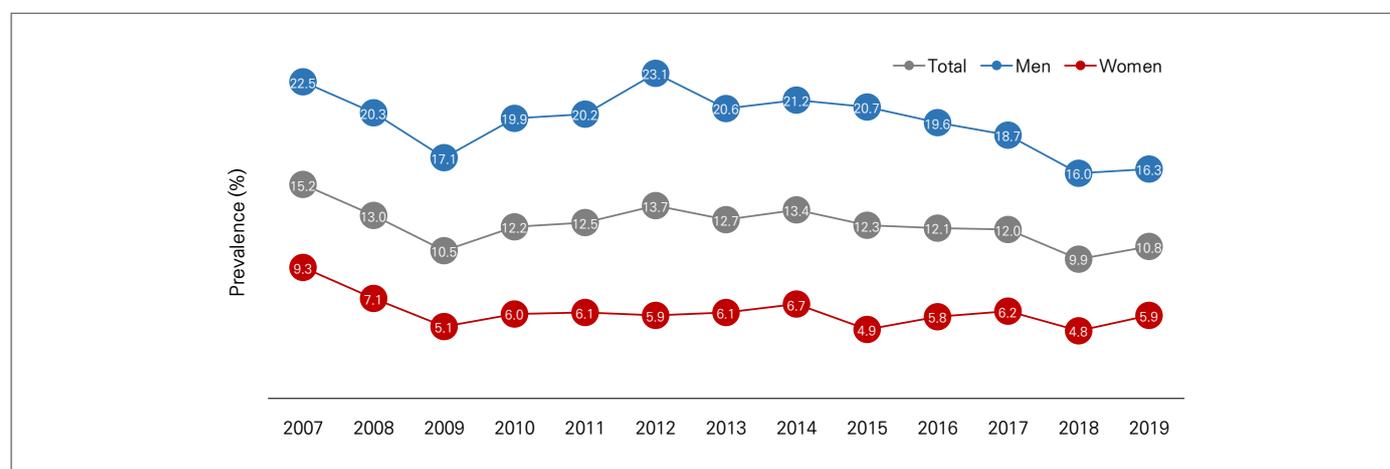
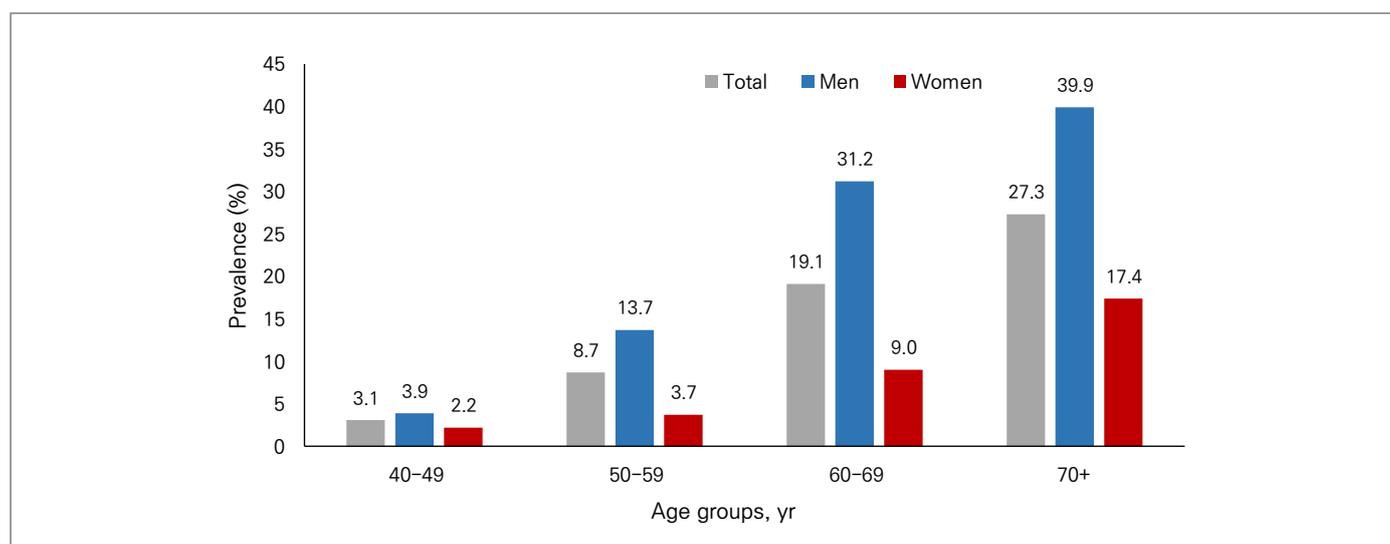
NCDs	Prevalence			Previously diagnosed			Treatment		
	2009	2015	2019	2007–2009	2013–2015	2019	2007–2009	2013–2015	2019
High blood pressure	26.3	27.8	27.2	66.3	67.3	71.4	60.3	63.6	67.1
Diabetes	11.6*	10.2	11.8	–	61.0	65.2	–	54.8	60.8
Hypercholesterolemia	11.4	17.9	22.3	38.8	57.7	61.7	26.9	45.5	53.1
COPD	10.5	12.3	10.8	–	–	2.5[§]	–	85.5[†]	84.5[‡]

Note: People aged 30 years or over(people aged 40 years or over with COPD)

* the year of 2011, § accumulated data during 2016–2018, † the continuous hospital utilization rate of COPD patients in 2014, ‡ the continuous hospital utilization rate of COPD patients in 2018 [11]

Source: 1) KDCA, 2019 National Health Statistics, 2020.

2) HIRA, Press Release, 28 May, 2020.

**Figure 1.** Prevalence rates of chronic obstructive pulmonary disease (COPD) among people aged 40 years or over in the Republic of Korea (ROK), 2007–2019 [9]**Figure 2.** Age-specific prevalence of chronic obstructive pulmonary disease (COPD) by gender in the Republic of Korea (ROK), 2019 [9]

주요 감염병 통계

1.1 환자감시 : 전수감시 감염병 주간 발생 현황 (15주차)

표 1. 2021년 15주차 보고 현황(2021. 4. 10. 기준)*

단위 : 보고환자수[†]

감염병*	금주	2021년 누계	5년간 주별 평균 [‡]	연간현황					금주 해외유입현황 : 국가명(신고수)
				2020	2019	2018	2017	2016	
제2급감염병									
결핵	450	5,596	515	19,933	23,821	26,433	28,161	30,892	
수두	368	5,098	1,142	31,372	82,868	96,467	80,092	54,060	
홍역	0	0	3	6	194	15	7	18	
콜레라	0	0	0	0	1	2	5	4	
장티푸스	1	38	3	42	94	213	128	121	
파라티푸스	1	11	1	64	55	47	73	56	
세균성이질	1	5	1	30	151	191	112	113	
장출혈성대장균감염증	1	19	1	281	146	121	138	104	
A형간염	99	1,339	153	3,939	17,598	2,437	4,419	4,679	
백일해	1	10	4	124	496	980	318	129	
유행성이하선염	205	2,416	345	9,913	15,967	19,237	16,924	17,057	
풍진	0	0	0	0	8	0	7	11	
수막구균 감염증	0	0	0	5	16	14	17	6	
폐렴구균 감염증	6	65	12	343	526	670	523	441	
한센병	0	1	0	3	4				
성홍열	13	229	313	2,245	7,562	15,777	22,838	11,911	
반코마이신내성황색 포도알균(VRSA) 감염증	0	0	0	9	3	0	0	-	
카바페뎀내성장내세균 속균종(CRE) 감염증	241	4,871	186	17,956	15,369	11,954	5,717	-	
E형간염	7	96	-	189	-	-	-	-	
제3급감염병									
파상풍	0	7	1	31	31	31	34	24	
B형간염	6	117	7	381	389	392	391	359	
일본뇌염	0	0	0	4	34	17	9	28	
C형간염	165	2,977	165	11,827	9,810	10,811	6,396	-	
말라리아	2	15	3	390	559	576	515	673	
레지오넬라증	3	79	4	354	501	305	198	128	
비브리오패혈증	0	0	0	70	42	47	46	56	
발진열	0	3	0	2	14	16	18	18	
쯔쯔가무시증	13	183	19	4,453	4,005	6,668	10,528	11,105	
렘토스피라증	5	24	1	135	138	118	103	117	
브루셀라증	0	2	0	8	1	5	6	4	
신증후군출혈열	3	47	4	274	399	433	531	575	
후천성면역결핍증(AIDS)	8	169	17	821	1,005	989	1,008	1,060	
크로이츠펠트-야콥병(CJD)	2	40	1	66	53	53	36	42	
뎅기열	0	0	3	42	273	159	171	313	
큐열	1	9	3	70	162	163	96	81	
라임병	0	0	0	8	23	23	31	27	
유비저	0	0	0	1	8	2	2	4	
치쿤구니야열	0	0	0	1	16	3	5	10	
중증열성혈소판감소 증후군(SFTS)	0	1	0	243	223	259	272	165	
지카바이러스감염증	0	0	0	0	3	3	11	16	

* 2020년·2021년 통계는 변동가능한 잠정통계이며, 2021년 누계는 1주부터 금주까지의 누계를 말함

† 각 감염병별로 규정된 신고범위(환자, 의사환자, 병원체보유자)의 모든 신고건을 포함함

‡ 미포함 질병: 에볼라바이러스병, 마버그열, 라싸열, 크리미안콩고출혈열, 남아메리카출혈열, 리프트밸리열, 두창, 페스트, 탄저, 보툴리눔독소증, 야토병, 신종감염병중후군, 중증급성호흡기중후군(SARS), 중증호흡기중후군(MERS), 동물인플루엔자 인체감염증, 신종인플루엔자, 디프테리아, 폴리오, b형헤모필루스인플루엔자, 발진티푸스, 공수병, 황열, 웨스트나일열, 진드기매개뇌염

§ 최근 5년(2016~2020년)의 해당 주의 신고 건수와 이전 2주, 이후 2주 동안의 신고 건수(총 25주) 평균임

표 2. 지역별 보고 현황(2021. 4. 10. 기준)(15주차)*

단위 : 보고환자수†

지역	제2급감염병											
	결핵			수두			홍역			콜레라		
	금주	2021년 누계	5년 누계 평균‡	금주	2021년 누계	5년 누계 평균‡	금주	2021년 누계	5년 누계 평균‡	금주	2021년 누계	5년 누계 평균‡
전국	450	5,596	7,443	368	5,098	17,463	0	0	29	0	0	0
서울	74	905	1,337	27	680	1,946	0	0	3	0	0	0
부산	26	368	514	16	343	1,012	0	0	1	0	0	0
대구	23	279	352	17	246	890	0	0	2	0	0	0
인천	14	284	398	26	281	908	0	0	1	0	0	0
광주	12	142	194	12	194	680	0	0	0	0	0	0
대전	12	130	163	12	141	476	0	0	3	0	0	0
울산	5	99	146	6	92	482	0	0	0	0	0	0
세종	3	35	27	0	57	163	0	0	12	0	0	0
경기	95	1,226	1,603	119	1,429	4,763	0	0	0	0	0	0
강원	15	233	322	15	143	464	0	0	1	0	0	0
충북	14	181	231	5	151	442	0	0	0	0	0	0
충남	22	291	353	19	196	675	0	0	1	0	0	0
전북	25	226	295	22	225	704	0	0	1	0	0	0
전남	26	321	385	18	240	725	0	0	1	0	0	0
경북	47	446	543	14	239	973	0	0	2	0	0	0
경남	28	365	479	35	354	1,649	0	0	1	0	0	0
제주	9	65	102	5	87	511	0	0	0	0	0	0

* 2021년 통계는 변동가능한 잠정통계임

† 각 감염병별로 규정된 신고범위(환자, 의사환자, 병원체보유자)의 모든 신고건을 포함함

‡ 최근 5년(2016~2020년)의 1주부터 해당 주까지 누계의 평균임

표 2. (계속) 지역별 보고 현황(2021. 4. 10. 기준)(15주차)*

단위 : 보고환자수†

지역	제2급감염병											
	장티푸스			파라티푸스			세균성이질			장출혈성대장균감염증		
	금주	2021년 누계	5년 누계 평균‡	금주	2021년 누계	5년 누계 평균‡	금주	2021년 누계	5년 누계 평균‡	금주	2021년 누계	5년 누계 평균‡
전국	1	38	49	1	11	10	1	5	38	1	19	13
서울	0	1	11	0	0	2	0	0	8	0	3	3
부산	0	5	5	0	4	1	0	0	2	0	0	0
대구	0	0	1	0	2	1	0	0	3	0	1	1
인천	0	1	4	0	0	1	0	0	3	0	1	1
광주	0	1	1	0	0	0	0	0	1	0	1	1
대전	0	2	2	0	0	0	0	0	1	0	1	0
울산	0	0	2	0	0	0	0	0	1	0	0	0
세종	0	0	1	0	0	0	0	0	0	0	1	0
경기	1	12	10	1	4	2	0	0	7	0	5	2
강원	0	0	2	0	0	0	0	0	1	0	1	1
충북	0	0	2	0	0	0	0	0	1	0	0	0
충남	0	1	2	0	0	0	0	0	2	0	0	0
전북	0	0	0	0	0	1	0	1	1	0	0	1
전남	0	1	1	0	1	1	1	3	2	0	0	1
경북	0	4	2	0	0	0	0	0	4	0	2	0
경남	0	10	3	0	0	1	0	0	1	0	2	1
제주	0	0	0	0	0	0	0	1	0	1	1	1

* 2021년 통계는 변동가능한 잠정통계임

† 각 감염병별로 규정된 신고범위(환자, 의사환자, 병원체보유자)의 모든 신고건을 포함함

‡ 최근 5년(2016~2020년)의 1주부터 해당 주까지 누계의 평균임

표 2. (계속) 지역별 보고 현황(2021. 4. 10. 기준)(15주차)*

단위 : 보고환자수†

지역	제2급감염병											
	A형간염			백일해			유행성이하선염			풍진		
	금주	2021년 누계	5년 누계 평균‡	금주	2021년 누계	5년 누계 평균‡	금주	2021년 누계	5년 누계 평균‡	금주	2021년 누계	5년 누계 평균‡
전국	99	1,339	1,541	1	10	92	205	2,416	3,675	0	0	1
서울	26	290	273	0	1	15	20	275	399	0	0	0
부산	2	22	60	0	0	4	10	149	220	0	0	0
대구	0	15	27	0	0	4	12	108	128	0	0	0
인천	4	99	114	1	1	8	9	111	169	0	0	0
광주	2	28	27	0	0	5	13	83	165	0	0	0
대전	2	40	149	0	0	3	5	78	99	0	0	0
울산	1	9	12	0	0	2	7	77	126	0	0	0
세종	0	8	22	0	0	3	0	13	19	0	0	0
경기	44	505	444	0	3	14	69	727	974	0	0	1
강원	0	19	31	0	0	0	5	88	136	0	0	0
충북	3	46	65	0	1	2	5	49	97	0	0	0
충남	7	106	121	0	0	2	11	108	161	0	0	0
전북	4	54	61	0	0	3	7	94	166	0	0	0
전남	4	42	43	0	0	8	10	108	159	0	0	0
경북	0	29	36	0	3	8	14	120	190	0	0	0
경남	0	12	48	0	1	10	7	181	416	0	0	0
제주	0	15	8	0	0	1	1	47	51	0	0	0

* 2021년 통계는 변동가능한 잠정통계임

† 각 감염병별로 규정된 신고범위(환자, 의사환자, 병원체보유자)의 모든 신고건을 포함함

‡ 최근 5년(2016~2020년)의 1주부터 해당 주까지 누계의 평균임

표 2. (계속) 지역별 보고 현황(2021. 4. 10. 기준)(15주차)*

단위 : 보고환자수[†]

지역	제2급감염병						제3급감염병					
	수막구균 감염증			성홍열			파상풍			B형간염		
	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]
전국	0	0	4	13	229	3,681	0	7	3	6	117	97
서울	0	0	1	2	31	506	0	1	0	1	12	17
부산	0	0	0	0	14	283	0	0	0	0	3	7
대구	0	0	0	1	3	112	0	2	0	1	3	3
인천	0	0	0	0	9	177	0	0	0	1	4	6
광주	0	0	0	4	29	194	0	0	0	0	5	2
대전	0	0	0	1	2	124	0	1	0	0	2	4
울산	0	0	0	1	10	174	0	0	0	0	2	2
세종	0	0	0	0	0	17	0	0	0	0	0	0
경기	0	0	1	2	63	1,020	0	1	0	2	45	25
강원	0	0	1	0	4	45	0	0	0	0	3	3
충북	0	0	0	1	4	66	0	0	0	0	1	2
충남	0	0	0	0	7	169	0	1	1	0	10	4
전북	0	0	0	0	5	128	0	0	0	0	3	4
전남	0	0	0	1	12	154	0	0	1	0	7	4
경북	0	0	0	0	9	187	0	1	0	0	6	5
경남	0	0	1	0	21	280	0	0	1	1	8	8
제주	0	0	0	0	6	45	0	0	0	0	3	1

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† 각 감염병별로 규정된 신고범위(환자, 의사환자, 병원체보유자)의 모든 신고건을 포함함

‡ 최근 5년(2016~2020년)의 1주부터 해당 주까지 누계의 평균임

표 2. (계속) 지역별 보고 현황(2021. 4. 10. 기준)(15주차)*

단위 : 보고환자수[†]

지역	제3급감염병											
	일본뇌염			말라리아			레지오넬라증			비브리오패혈증		
	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]
전국	0	0	0	2	15	18	3	79	69	0	0	0
서울	0	0	0	0	1	6	1	12	21	0	0	0
부산	0	0	0	0	1	0	0	2	4	0	0	0
대구	0	0	0	0	0	0	0	6	3	0	0	0
인천	0	0	0	1	1	2	0	2	5	0	0	0
광주	0	0	0	0	0	1	0	1	1	0	0	0
대전	0	0	0	0	0	0	0	1	1	0	0	0
울산	0	0	0	0	0	0	0	2	1	0	0	0
세종	0	0	0	0	0	0	0	0	0	0	0	0
경기	0	0	0	1	10	8	1	15	16	0	0	0
강원	0	0	0	0	1	1	0	2	2	0	0	0
충북	0	0	0	0	0	0	0	2	2	0	0	0
충남	0	0	0	0	1	0	0	1	2	0	0	0
전북	0	0	0	0	0	0	0	8	2	0	0	0
전남	0	0	0	0	0	0	0	6	2	0	0	0
경북	0	0	0	0	0	0	0	1	5	0	0	0
경남	0	0	0	0	0	0	1	4	2	0	0	0
제주	0	0	0	0	0	0	0	14	0	0	0	0

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† 각 감염병별로 규정된 신고범위(환자, 의사환자, 병원체보유자)의 모든 신고건을 포함함

‡ 최근 5년(2016~2020년)의 1주부터 해당 주까지 누계의 평균임

표 2. (계속) 지역별 보고 현황(2021. 4. 10. 기준)(15주차)*

단위 : 보고환자수[†]

지역	제3급감염병											
	발진열			쯔쯔가무시증			렙토스피라증			브루셀라증		
	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]
전국	0	3	0	13	183	189	5	24	8	0	2	0
서울	0	0	0	0	8	9	0	0	1	0	0	0
부산	0	0	0	0	9	9	0	3	0	0	0	0
대구	0	0	0	0	8	1	0	0	0	0	0	0
인천	0	1	0	0	2	5	0	3	0	0	0	0
광주	0	0	0	0	5	3	0	0	1	0	0	0
대전	0	0	0	0	2	3	0	1	0	0	0	0
울산	0	0	0	0	3	6	0	0	0	0	0	0
세종	0	0	0	0	0	1	0	0	0	0	0	0
경기	0	1	0	2	10	17	1	2	2	0	2	0
강원	0	0	0	0	2	5	2	5	0	0	0	0
충북	0	0	0	0	2	4	1	2	0	0	0	0
충남	0	0	0	0	8	16	0	3	1	0	0	0
전북	0	0	0	5	46	15	0	2	1	0	0	0
전남	0	0	0	3	48	44	1	2	1	0	0	0
경북	0	0	0	0	5	12	0	1	1	0	0	0
경남	0	0	0	3	20	34	0	0	0	0	0	0
제주	0	1	0	0	5	5	0	0	0	0	0	0

* 2021년 통계는 변동가능한 잠정통계임

† 각 감염병별로 규정된 신고범위(환자, 의사환자, 병원체보유자)의 모든 신고건을 포함함

‡ 최근 5년(2016~2020년)의 1주부터 해당 주까지 누계의 평균임

표 2. (계속) 지역별 보고 현황(2021. 4. 10. 기준)(15주차)*

단위 : 보고환자수[†]

지역	제3급감염병											
	신증후군출혈열			크로이츠펠트-야콥병(CJD)			뎅기열			큐열		
	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]	금주	2021년 누계	5년 누계 평균 [‡]
전국	3	47	58	2	40	11	0	0	50	1	9	26
서울	0	1	3	1	5	3	0	0	15	0	1	1
부산	0	0	1	0	4	0	0	0	4	0	0	1
대구	0	2	0	0	3	1	0	0	3	0	0	1
인천	0	1	1	0	3	0	0	0	3	0	0	0
광주	0	2	1	0	1	0	0	0	0	0	0	1
대전	0	0	0	0	1	0	0	0	0	0	0	1
울산	0	0	0	0	0	0	0	0	1	0	0	1
세종	0	0	0	0	0	0	0	0	0	0	0	0
경기	0	8	18	0	11	3	0	0	15	0	1	4
강원	0	3	3	0	3	1	0	0	1	0	0	0
충북	0	1	3	0	0	0	0	0	1	0	0	5
충남	0	8	5	1	2	0	0	0	2	1	5	3
전북	1	11	5	0	2	1	0	0	0	0	0	3
전남	0	4	6	0	0	0	0	0	1	0	1	2
경북	2	4	8	0	1	1	0	0	1	0	1	1
경남	0	2	3	0	3	1	0	0	2	0	0	2
제주	0	0	1	0	1	0	0	0	1	0	0	0

* 2021년 통계는 변동가능한 잠정통계임

† 각 감염병별로 규정된 신고범위(환자, 의사환자, 병원체보유자)의 모든 신고건을 포함함

‡ 최근 5년(2016~2020년)의 1주부터 해당 주까지 누계의 평균임

표 2. (계속) 지역별 보고 현황(2021. 4. 10. 기준)(15주차)*

단위 : 보고환자수†

지역	제3급감염병								
	라임병			중증열성혈소판감소증후군(SFTS)			지카바이러스감염증		
	금주	2021년 누계	5년 누계 평균‡	금주	2021년 누계	5년 누계 평균‡	금주	2021년 누계	5년 누계 평균‡
전국	0	0	1	0	1	0	0	0	-
서울	0	0	1	0	0	0	0	0	-
부산	0	0	0	0	0	0	0	0	-
대구	0	0	0	0	0	0	0	0	-
인천	0	0	0	0	0	0	0	0	-
광주	0	0	0	0	0	0	0	0	-
대전	0	0	0	0	0	0	0	0	-
울산	0	0	0	0	0	0	0	0	-
세종	0	0	0	0	0	0	0	0	-
경기	0	0	0	0	0	0	0	0	-
강원	0	0	0	0	0	0	0	0	-
충북	0	0	0	0	0	0	0	0	-
충남	0	0	0	0	0	0	0	0	-
전북	0	0	0	0	0	0	0	0	-
전남	0	0	0	0	0	0	0	0	-
경북	0	0	0	0	0	0	0	0	-
경남	0	0	0	0	1	0	0	0	-
제주	0	0	0	0	0	0	0	0	-

* 2021년 통계는 변동가능한 잠정통계임

† 각 감염병별로 규정된 신고범위(환자, 의사환자, 병원체보유자)의 모든 신고건을 포함함

‡ 최근 5년(2016~2020년)의 1주부터 해당 주까지 누계의 평균임

1.2 환자감시 : 표본감시 감염병 주간 발생 현황 (15주차)

1. 인플루엔자 주간 발생 현황(15주차, 2021. 4. 10. 기준)

- 2021년도 제15주 인플루엔자 표본감시(전국 200개 표본감시기관) 결과, 의사환자분율은 외래환자 1,000명당 2.3명으로 지난주(2.5명) 대비 감소

※ 2020-2021절기 유행기준은 5.8명/(1,000)

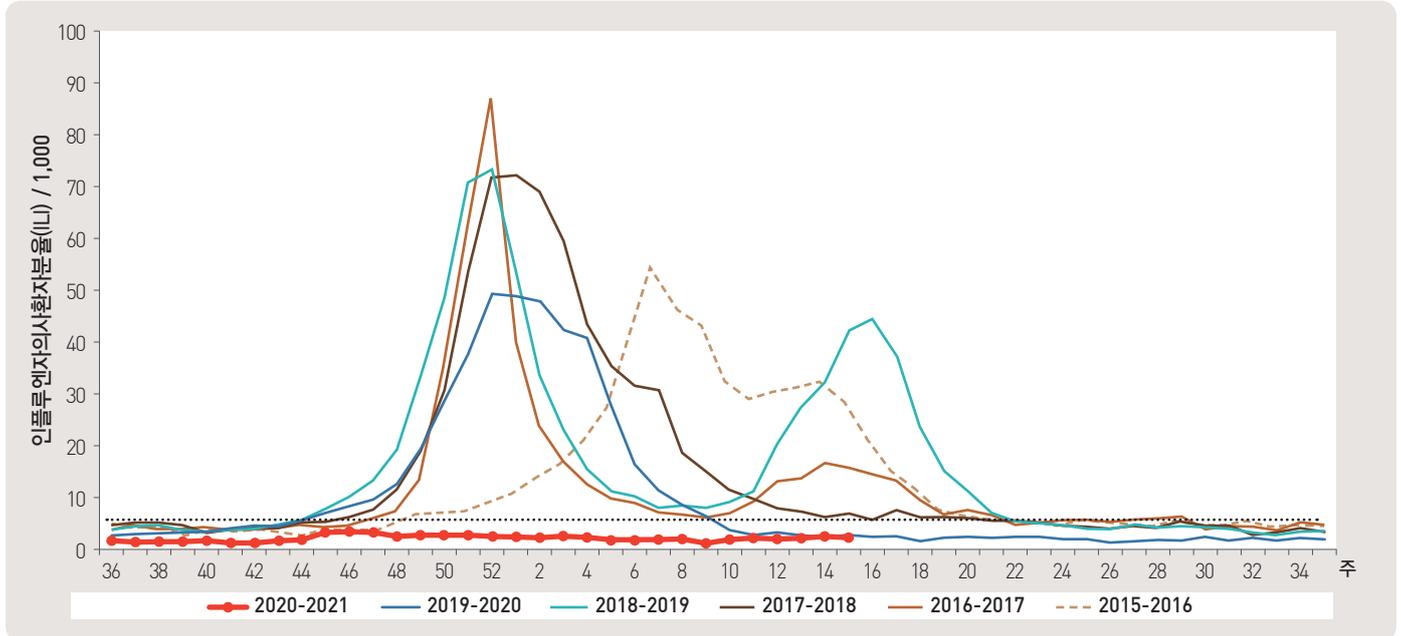


그림 1. 외래 환자 1,000명당 인플루엔자 의사환자 발생 현황

2. 수족구 발생 주간 현황(15주차, 2021. 4. 10. 기준)

- 2021년도 제15주차 수족구병 표본감시(전국 97개 의료기관) 결과, 의사환자 분율은 외래환자 1,000명당 0.2명으로 전주 0.3명 대비 감소

※ 수족구병은 2009년 6월 법정감염병으로 지정되어 표본감시체제로 운영

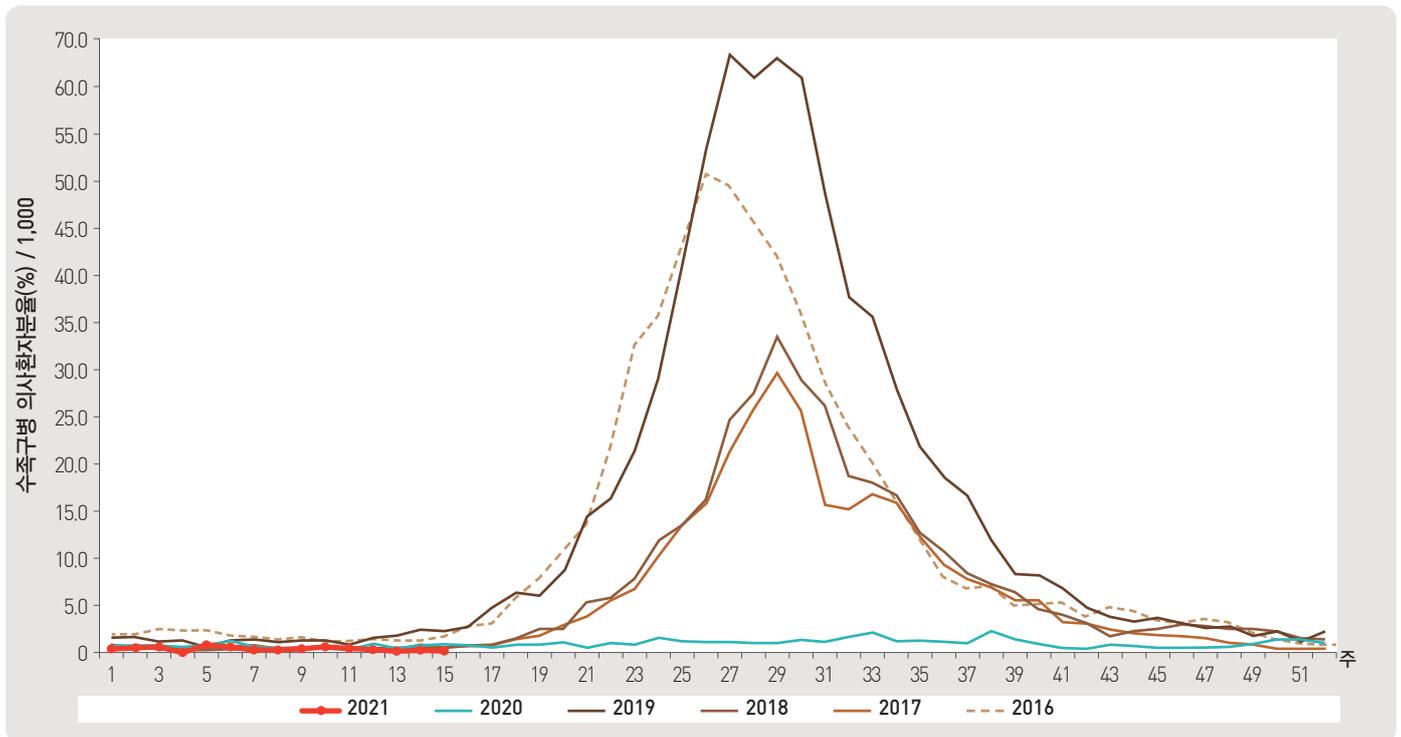


그림 2. 외래 환자 1,000명당 수족구 발생 현황

▶ 자세히 보기 : 질병관리청 → 간행물·통계 → 감염병발생정보 → 표본감시주간소식지

3. 안과 감염병 주간 발생 현황(15주차, 2021. 4. 10. 기준)

- 2021년도 제15주차 유행성각결막염 표본감시(전국 90개 의료기관) 결과, 외래환자 1,000명당 분율은 3.9명으로 전주 3.6명 대비 증가
- 동기간 급성출혈성결막염의 환자 분율은 0.3명으로 전주 0.2명 대비 증가

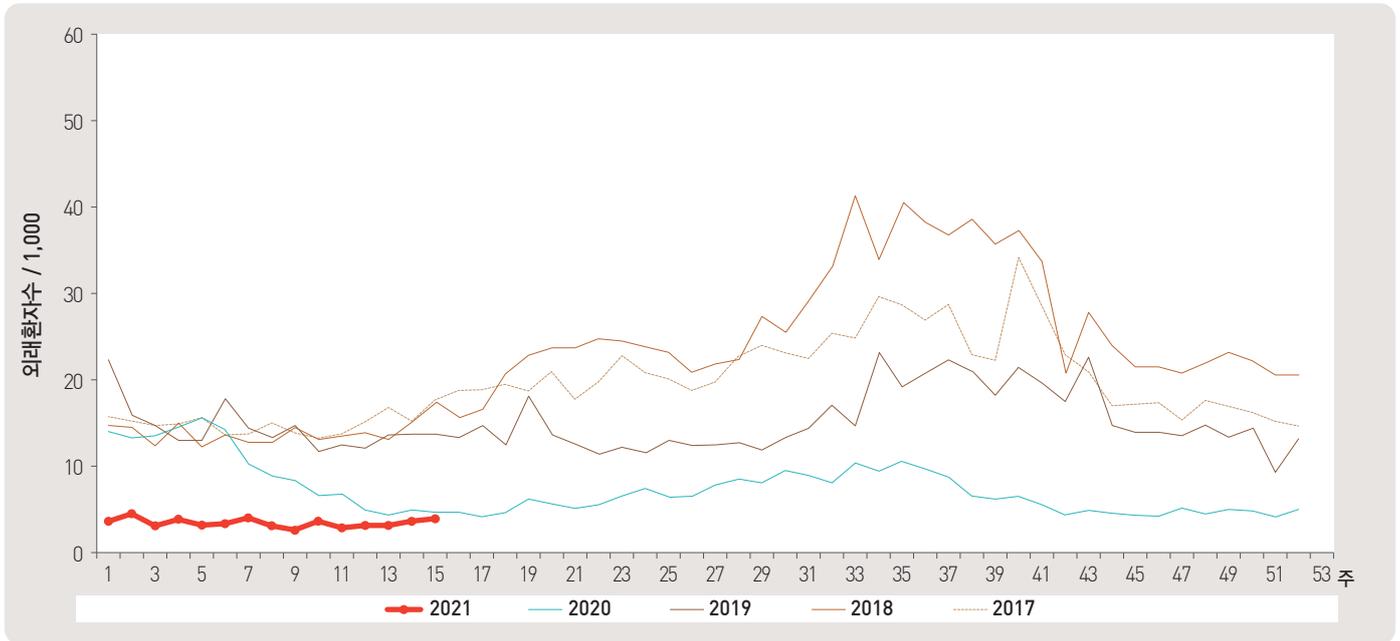


그림 3. 외래 환자 1,000명당 유행성각결막염 발생 현황

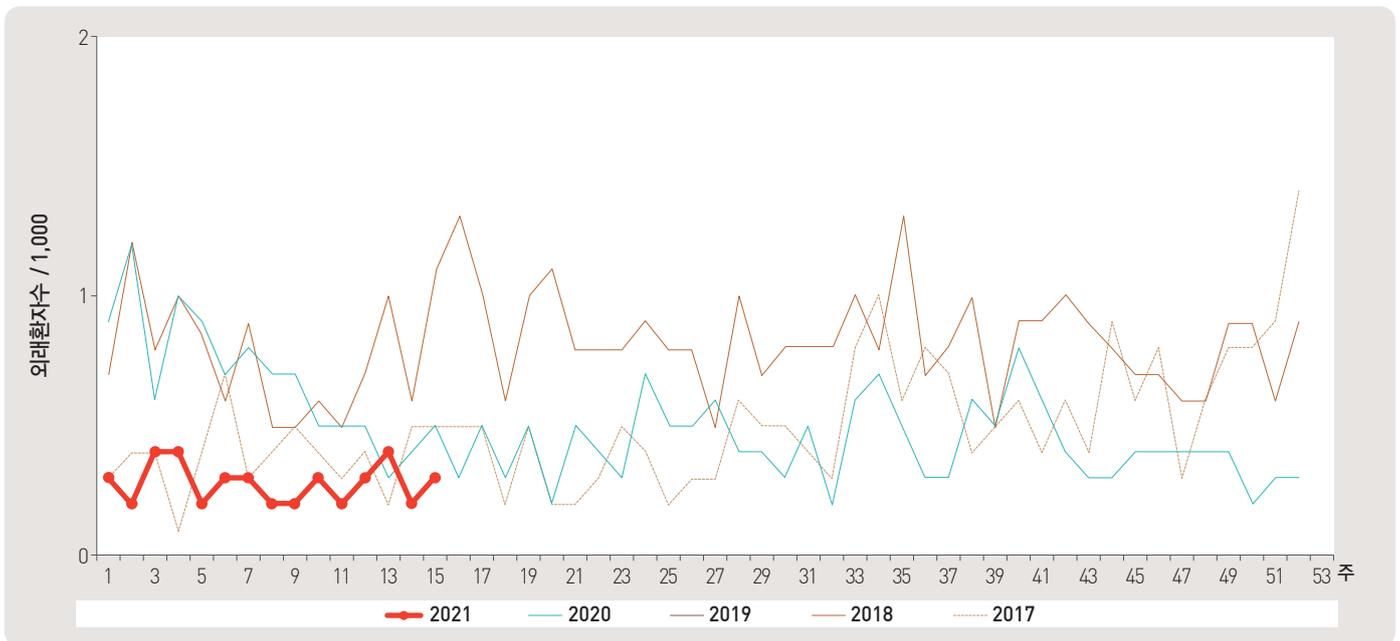


그림 4. 외래 환자 1,000명당 급성출혈성결막염 발생 현황

4. 성매개감염병 주간 발생 현황(15주차, 2021. 4. 10. 기준)

- 2021년도 제15주 성매개감염병 표본감시기관(전국 보건소 및 의료기관 588개 참여)에서 신고기관 당 사람유두종바이러스 감염증 3.8건, 성기단순포진 2.4건, 침규콘딜롬 2.1건, 클라미디아감염증 1.9건, 임질 1.2건, 1기 매독 1.0건, 2기 매독 1.0건, 선천성 매독 0.0건을 신고함.

* 제15주차 신고의료기관 수: 임질 15개, 클라미디아감염증 47개, 성기단순포진 42개, 침규콘딜롬 32개, 사람유두종바이러스 감염증 42개, 1기 매독 4개, 2기 매독 2개, 선천성 매독 0개
 ** 2020.1.1.일부터 사람유두종바이러스 감염증이 표본감시에 신설되었으며, 매독이 전수감시에서 표본감시로 변경됨

단위 : 신고수/신고기관 수

임질			클라미디아 감염증			성기단순포진			침규콘딜롬		
금주	2020년 누적	최근 5년 누적 평균 [§]	금주	2020년 누적	최근 5년 누적 평균 [§]	금주	2020년 누적	최근 5년 누적 평균 [§]	금주	2020년 누적	최근 5년 누적 평균 [§]
1.2	3.5	4.2	1.9	9.1	11.2	2.4	14.4	14.4	2.1	8.8	8.7

사람유두종바이러스감염증			1기 매독			2기 매독			선천성		
금주	2020년 누적	최근 5년 누적 평균 [§]	금주	2020년 누적	최근 5년 누적 평균 [§]	금주	2020년 누적	최근 5년 누적 평균 [§]	금주	2020년 누적	최근 5년 누적 평균 [§]
3.8	33.1	4.9	1.0	1.4	0.3	1.0	1.4	0.3	0.0	1.0	0.2

누계 : 매년 첫 주부터 금주까지의 보고 누계

† 각 질병별로 규정된 신고 범위(환자, 의사환자, 병원체보유자)의 모든 신고 건을 포함

§ 최근 5년('16-'20) 누적 평균(Cum, 5-year average) : 최근 5년 1주차부터 금주까지 누적 환자 수 평균

1.3 수인성 및 식품매개 감염병 집단발생 주간 현황 (15주차)

▣ 수인성 및 식품매개 감염병 집단발생 주간 현황(15주차, 2021. 4. 10. 기준)

- 2021년도 제15주에 집단발생이 9건(사례수 117명) 발생하였으며 누적발생건수는 121건(사례수 1,881명)이 발생함.

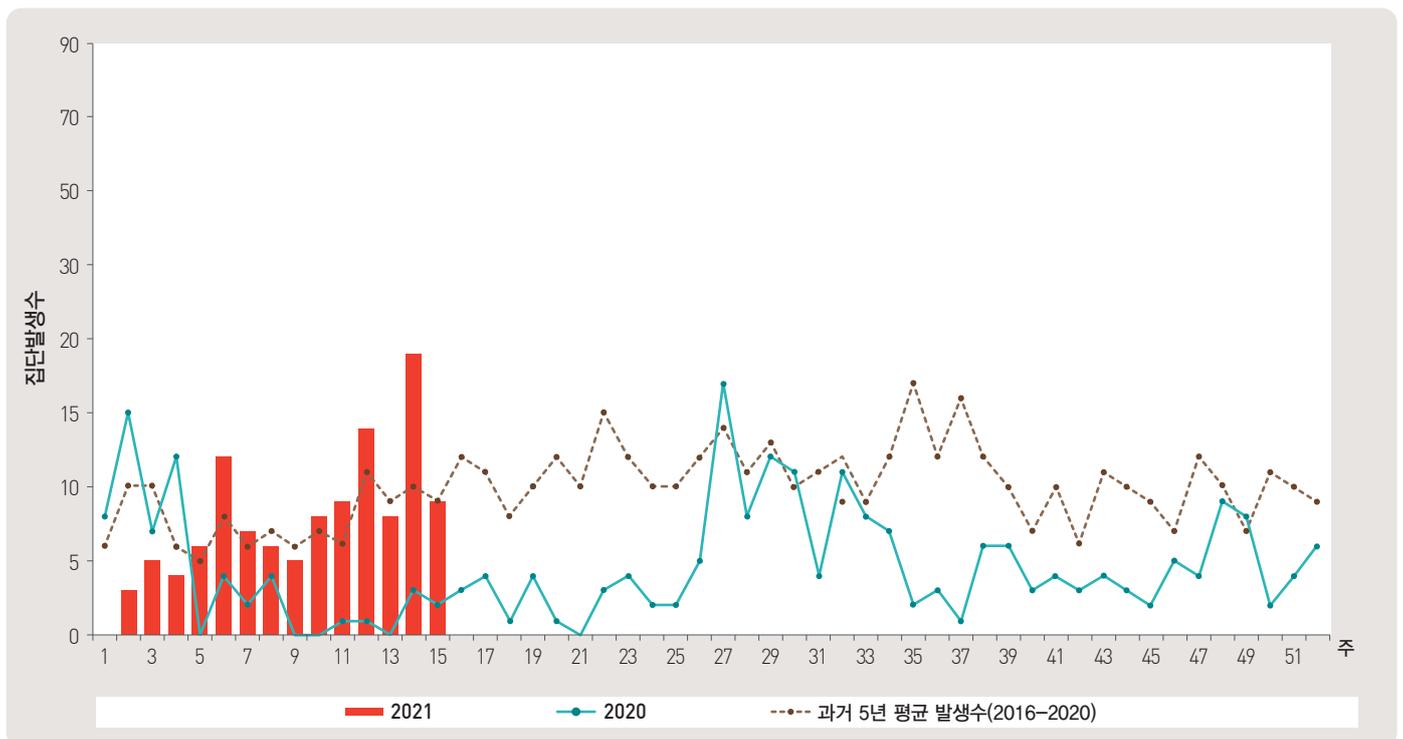


그림 5. 수인성 및 식품매개 감염병 집단발생 현황

2.1 병원체감시 : 인플루엔자 및 호흡기바이러스 주간 감시 현황(15주차)

1. 인플루엔자 바이러스 주간 현황(15주차, 2021. 4. 10. 기준)

- 2021년도 제15주에 전국 52개 감시사업 참여의료기관에서 의뢰된 호흡기검체 122건 중 양성 없음.

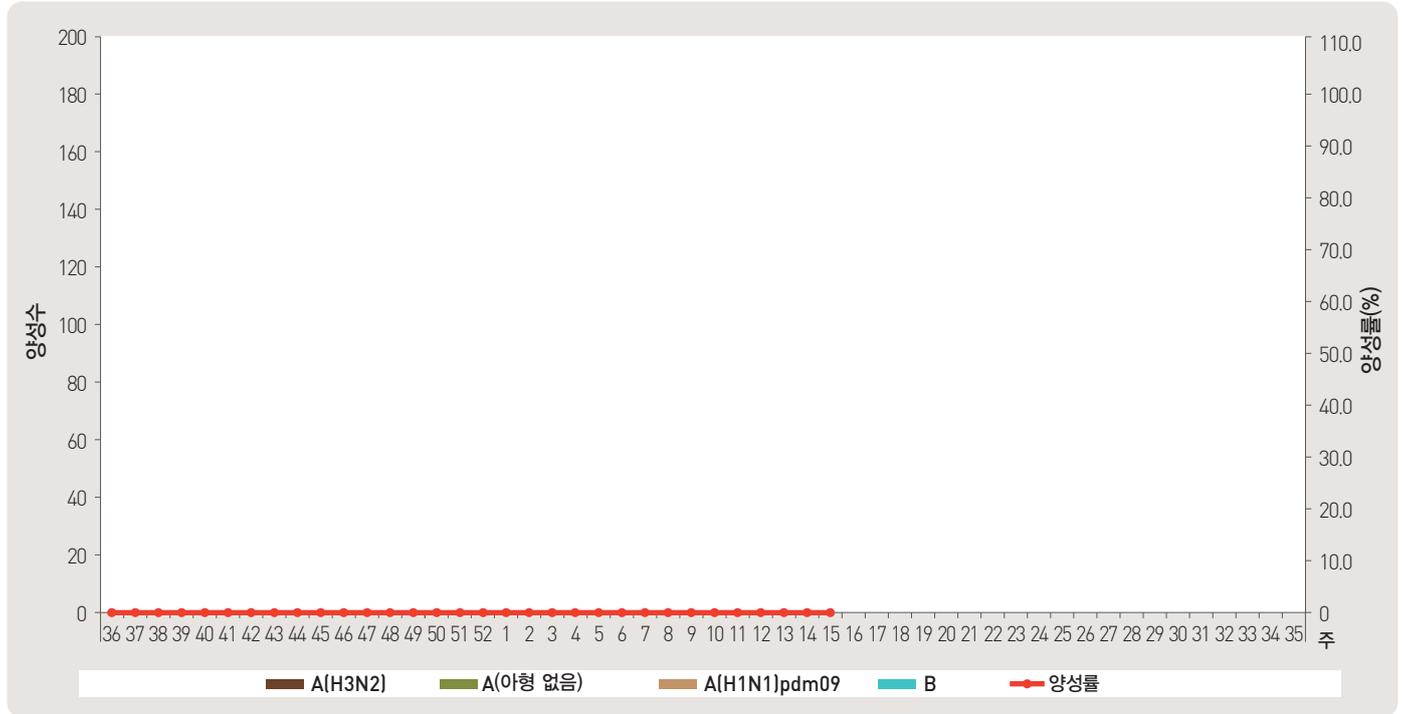


그림 6. 인플루엔자 바이러스 검출 현황

2. 호흡기 바이러스 주간 현황(15주차, 2021. 4. 10. 기준)

- 2021년도 제15주 호흡기 검체에 대한 유전자 검사결과 66.4%의 호흡기 바이러스가 검출되었음.
(최근 4주 평균 113개의 호흡기 검체에 대한 유전자 검사결과를 나타내고 있음)

※ 주별통계는 잠정통계이므로 변동가능

2021 (주)	주별		검출률 (%)							
	검체 건수	검출률 (%)	아데노 바이러스	파라 인플루엔자 바이러스	호흡기 세포융합 바이러스	인플루엔자 바이러스	코로나 바이러스	리노 바이러스	보카 바이러스	메타뉴모 바이러스
12	112	63.4	7.1	0.0	0.0	0.0	0.0	49.1	7.1	0.0
13	109	64.2	2.8	0.0	0.0	0.0	0.0	48.6	12.8	0.0
14	109	55.0	4.6	0.0	0.0	0.0	0.0	42.2	8.3	0.0
15	122	66.4	6.6	0.0	0.0	0.0	0.0	47.5	12.3	0.0
Cum. ※	452	62.4	5.3	0.0	0.0	0.0	0.0	46.9	10.2	0.0
2020 Cum. ▼	5,819	48.6	6.5	0.4	3.1	12.0	3.4	18.4	3.5	1.4

※ 4주 누적 : 2021년 3월 14일 - 2021년 4월 10일 검출률임 (지난 4주간 평균 113개의 검체에에서 검출된 수의 평균).

▼ 2020년 누적 : 2019년 12월 29일 - 2020년 12월 26일 검출률임.

▶ 자세히 보기 : 질병관리청 → 간행물·통계 → 감염병발생정보 → 표본감시주간소식지

2.2 병원체감시 : 급성설사질환 바이러스 및 세균 주간 감시 현황 (14주차)

▣ 급성설사질환 바이러스 및 세균 주간 검출 현황(14주차, 2021. 4. 3. 기준)

- 2021년도 제14주 실험실 표본감시(17개 시·도 보건환경연구원 및 70개 의료기관) 급성설사질환 원인 바이러스 검출 건수는 26건(38.2%), 세균 검출 건수는 14건(10.5%) 이었음.

◆ 급성설사질환 바이러스

주	검체수	검출 건수(검출률, %)						
		노로바이러스	그룹 A 로타바이러스	장내 아데노바이러스	아스트로바이러스	사포바이러스	합계	
2021	11	65	19(29.2)	0(0.0)	0(0.0)	2(3.1)	0(0.0)	21(32.3)
	12	73	21(28.8)	0(0.0)	1(1.4)	5(6.8)	0(0.0)	27(37.0)
	13	73	24(32.9)	1(1.4)	0(0.0)	2(2.7)	0(0.0)	27(37.0)
	14	68	19(27.9)	2(2.9)	0(0.0)	5(7.4)	0(0.0)	26(38.2)
2021년 누적	985	343(34.8)	20(2.0)	8(0.8)	15(1.5)	2(0.2)	388(39.4)	

* 검체는 5세 이하 아동의 급성설사 질환자에게서 수집됨.

◆ 급성설사질환 세균

주	검체수	분리 건수(분리율, %)										
		살모넬라균	병원성 대장균	세균성 이질균	장염 비브리오균	비브리오 콜레라균	캠필로 박터균	클라스트리дум 퍼프린젠스	황색 포도알균	바실러스 세레우스균	합계	
2021	11	180	3 (1.7)	2 (1.1)	0 (0.0)	0 (0.0)	0 (0.0)	2 (1.1)	4 (2.2)	10 (5.6)	3 (1.7)	25 (13.9)
	12	204	4 (2.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	3 (1.5)	7 (3.4)	10 (4.9)	5 (2.5)	30 (14.7)
	13	205	4 (2.0)	2 (1.0)	1 (0.5)	0 (0.0)	0 (0.0)	1 (0.5)	6 (2.9)	8 (3.9)	1 (0.5)	23 (11.2)
	14	133	3 (2.3)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	2 (1.5)	1 (0.8)	3 (2.3)	4 (3.0)	14 (10.5)
2021년 누적	2,690	32 (1.0)	35 (1.3)	1 (0.04)	0 (0.0)	0 (0.0)	25 (0.9)	61 (2.3)	99 (3.7)	36 (1.3)	293 (10.9)	

* 2020년 실험실 감시체계 참여기관(69개 의료기관)

▶ 자세히 보기 : 질병관리청 → 간행물·통계 → 감염병발생정보 → 표본감시주간소식지 → 감염병포털 → 실험실소식지

2.3 병원체감시 : 엔테로바이러스 주간 감시 현황 (14주차)

▣ 엔테로바이러스 주간 검출 현황(14주차, 2021. 4. 3. 기준)

- 2021년도 제14주 실험실 표본감시(17개 시·도 보건환경연구원, 전국 60개 참여병원) 결과, 엔테로바이러스 검출률 0.0%(0건 양성/8검체), 2021년 누적 양성률 0.7%(1건 양성/134검체).
- 무균성수막염 0건(2021년 누적 1건), 수족구병 및 포진성구협염 0건(2021년 누적 0건), 합병증 동반 수족구 0건(2021년 누적 0건), 기타 0건(2021년 누적 0건)임.

◆ 무균성수막염

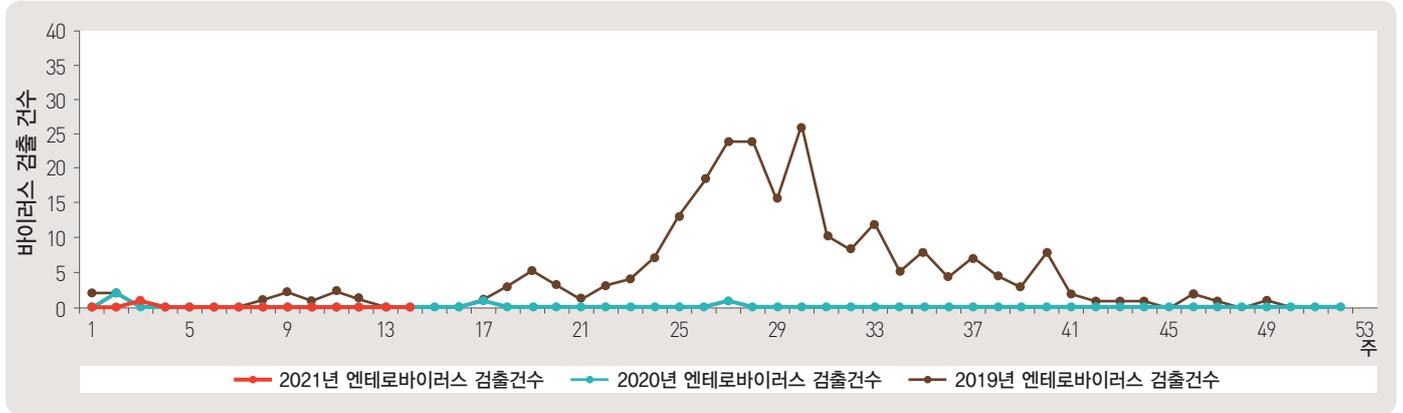


그림 7. 무균성수막염 바이러스 검출수

◆ 수족구병 및 포진성구협염

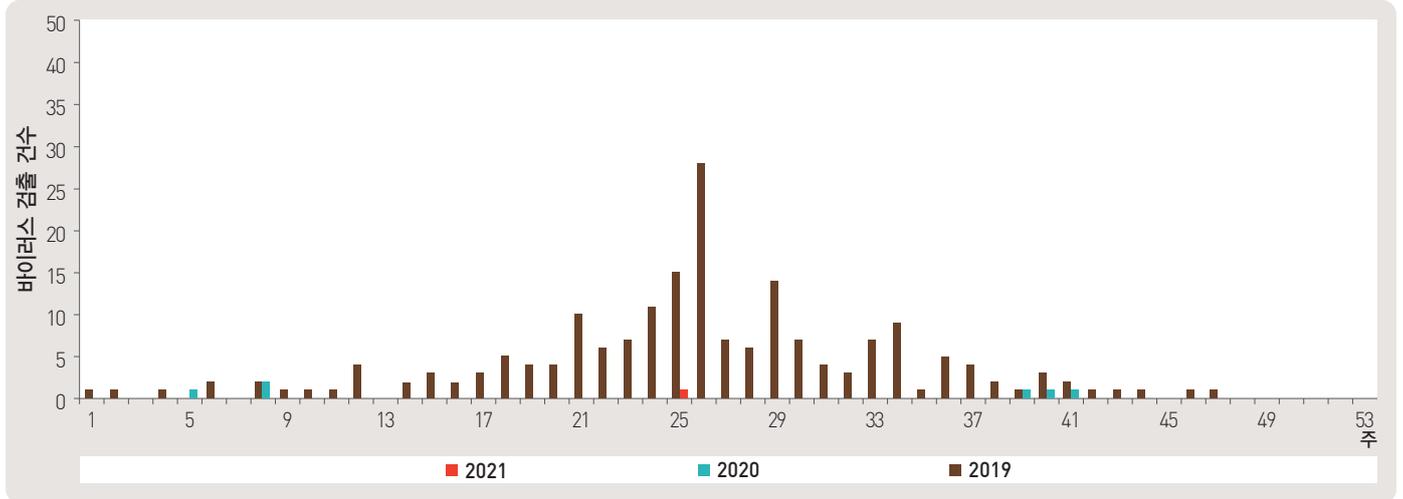


그림 8. 수족구 및 포진성구협염 바이러스 검출수

◆ 합병증 동반 수족구

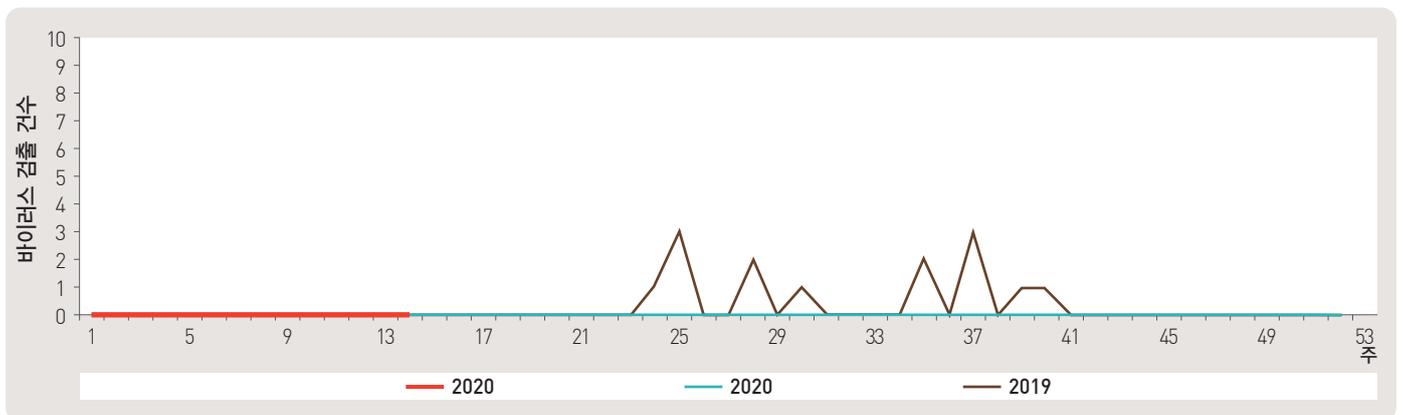


그림 9. 합병증 동반 수족구 바이러스 검출수

▶ 자세히 보기 : 질병관리청 → 간행물·통계 → 감염병발생정보 → 표본감시주간소식지 → 감염병포털 → 실험실소식지

3.1 매개체감시 / 말라리아 매개모기 주간 감시현황 (14주차)

▣ 말라리아 매개모기 주간 검출 현황(14주차, 2021. 4. 3. 기준)

- 2021년도 제14주 말라리아 매개모기 주간 발생현황(3개 시·도, 총 50개 채집지점)
 - 전체모기 : 평균 1개체 평년 0개체 대비 1개체 증가
 - 말라리아 매개모기 : 평균 0개체 전년 0개체와 동일
- ※ 모기수 산출법 : 1주일간 유문등에 채집된 모기의 평균수(개체수/트랩/일)
- ※ 2020년에는 보건소·보건환경연구원의 현안업무(코로나바이러스감염증-19) 대응으로 14주차 미채집

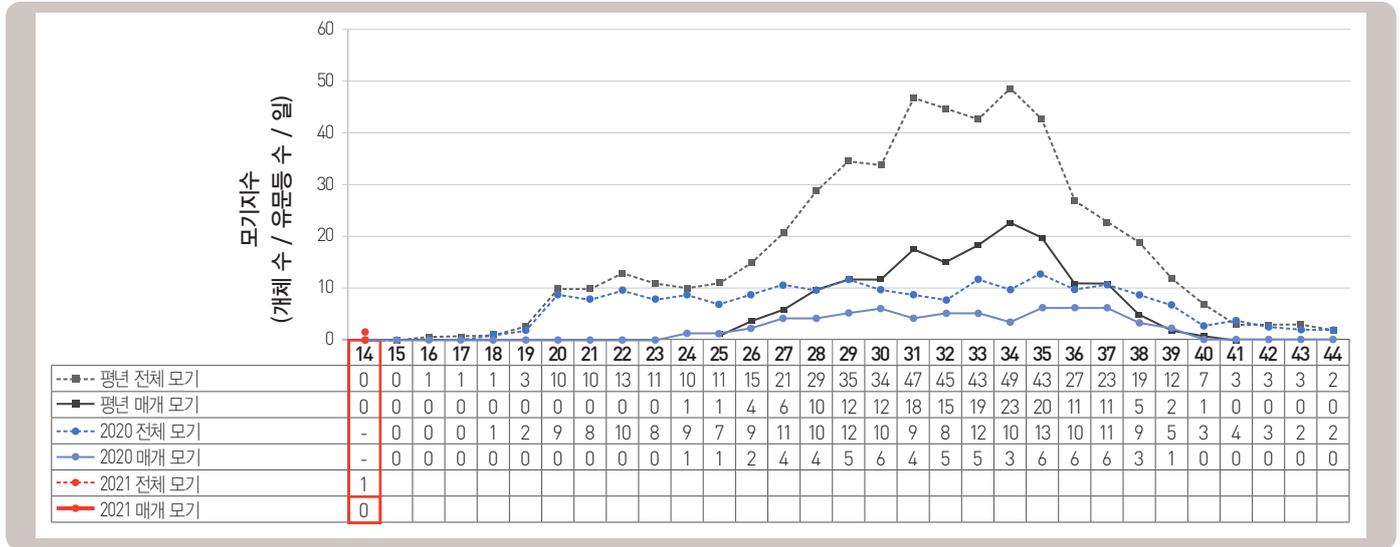


그림 10. 말라리아 매개모기 검출수

3.2 매개체감시 / 일본뇌염 매개모기 주간 발생 현황 (15주차)

▣ 일본뇌염 매개모기 주간 발생 현황 (15주차, 2021. 4. 10. 기준)

- 2021년 제15주 일본뇌염 매개모기 주간 발생현황 : 9개 시·도 보건환경연구원(총 9개 지점)
 - 전체모기 수 : 평균 3개체 [평년 2개체 대비 1개체 및 전년 1개체 대비 2개체 증가]
 - 일본뇌염 매개모기 : 평균 1개체 [평년 및 전년 0개체 대비 1개체 증가]

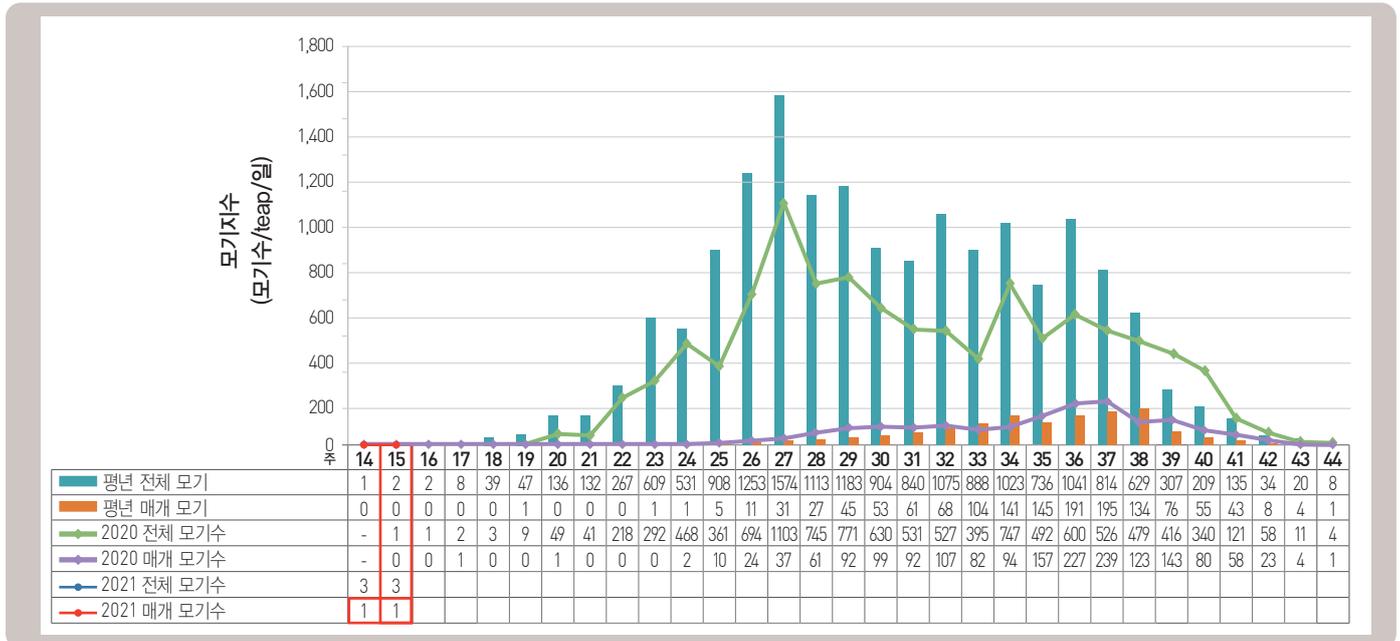


그림 11. 일본뇌염 매개모기 주간 발생 현황

주요 통계 이해하기

〈통계표 1〉은 지난 5년간 발생한 법정감염병과 2021년 해당 주 발생현황을 비교한 표로, 금주 환자 수(Current week)는 2021년 해당 주의 신고건수를 나타내며, 2021년 누계 환자수(Cum, 2021)는 2021년 1주부터 해당 주까지의 누계 건수, 그리고 5년 주 평균 환자수(5-year weekly average)는 지난 5년(2016-2020년) 해당 주의 신고건수와 이전 2주, 이후 2주의 신고건수(총 25주) 평균으로 계산된다. 그러므로 금주 환자수(Current week)와 5년 주 평균 환자수(5-year weekly average)의 신고건수를 비교하면 해당 주 단위 시점과 예년의 신고 수준을 비교해 볼 수 있다. 연도별 환자수(Total no. of cases by year)는 지난 5년간 해당 감염병 현황을 나타내는 확정 통계이며 연도별 현황을 비교해 볼 수 있다.

예) 2021년 12주의 5년 주 평균 환자수(5-year weekly average)는 2016년부터 2020년의 11주부터 14주까지의 신고 건수를 총 25주로 나눈 값으로 구해진다.

$$* \text{5년 주 평균 환자수(5-year weekly average)} = (X1 + X2 + \dots + X25) / 25$$

	11주	11주	12주	13주	14주
2021년			해당 주		
2020년	X1	X2	X3	X4	X5
2019년	X6	X7	X8	X9	X10
2018년	X11	X12	X13	X14	X15
2017년	X16	X17	X18	X19	X20
2016년	X21	X22	X23	X24	X25

〈통계표 2〉는 17개 시·도 별로 구분한 법정감염병 보고 현황을 보여 주고 있으며, 각 감염병별로 최근 5년 누계 평균 환자수(Cum, 5-year average)와 2021년 누계 환자수(Cum, 2021)를 비교해 보면 최근까지의 누적 신고건수에 대한 이전 5년 동안 해당 주까지의 평균 신고건수와 비교가 가능하다. 최근 5년 누계 평균 환자수(Cum, 5-year average)는 지난 5년(2016-2020년) 동안의 동기간 신고 누계 평균으로 계산된다.

기타 표본감시 감염병에 대한 신고현황 그림과 통계는 최근 발생양상을 신속하게 파악하는데 도움이 된다.

Statistics of selected infectious diseases

Table 1. Reported cases of national infectious diseases in Republic of Korea, week ending April 10, 2021 (15th week)*

Unit: No. of cases[†]

Classification of disease †	Current week	Cum. 2021	5-year weekly average	Total no. of cases by year					Imported cases of current week : Country (no. of cases)
				2020	2019	2018	2017	2016	
Category II									
Tuberculosis	450	5,596	515	19,933	23,821	26,433	28,161	30,892	
Varicella	368	5,098	1,142	31,372	82,868	96,467	80,092	54,060	
Measles	0	0	3	6	194	15	7	18	
Cholera	0	0	0	0	1	2	5	4	
Typhoid fever	1	38	3	42	94	213	128	121	
Paratyphoid fever	1	11	1	64	55	47	73	56	
Shigellosis	1	5	1	30	151	191	112	113	
EHEC	1	19	1	281	146	121	138	104	
Viral hepatitis A	99	1,339	153	3,939	17,598	2,437	4,419	4,679	
Pertussis	1	10	4	124	496	980	318	129	
Mumps	205	2,416	345	9,913	15,967	19,237	16,924	17,057	
Rubella	0	0	0	0	8	0	7	11	
Meningococcal disease	0	0	0	5	16	14	17	6	
Pneumococcal disease	6	65	12	343	526	670	523	441	
Hansen's disease	0	1	0	3	4				
Scarlet fever	13	229	313	2,245	7,562	15,777	22,838	11,911	
VRSA	0	0	0	9	3	0	0	-	
CRE	241	4,871	186	17,956	15,369	11,954	5,717	-	
Viral hepatitis E	7	96	-	189	-	-	-	-	
Category III									
Tetanus	0	7	1	31	31	31	34	24	
Viral hepatitis B	6	117	7	381	389	392	391	359	
Japanese encephalitis	0	0	0	4	34	17	9	28	
Viral hepatitis C	165	2,977	165	11,827	9,810	10,811	6,396	-	
Malaria	2	15	3	390	559	576	515	673	
Legionellosis	3	79	4	354	501	305	198	128	
Vibrio vulnificus sepsis	0	0	0	70	42	47	46	56	
Murine typhus	0	3	0	2	14	16	18	18	
Scrub typhus	13	183	19	4,453	4,005	6,668	10,528	11,105	
Leptospirosis	5	24	1	135	138	118	103	117	
Brucellosis	0	2	0	8	1	5	6	4	
HFRS	3	47	4	274	399	433	531	575	
HIV/AIDS	8	169	17	821	1,005	989	1,008	1,060	
CJD	2	40	1	66	53	53	36	42	
Dengue fever	0	0	3	42	273	159	171	313	
Q fever	1	9	3	70	162	163	96	81	
Lyme Borreliosis	0	0	0	8	23	23	31	27	
Melioidosis	0	0	0	1	8	2	2	4	
Chikungunya fever	0	0	0	1	16	3	5	10	
SFTS	0	1	0	243	223	259	272	165	
Zika virus infection	0	0	0	0	3	3	11	16	

Abbreviation: EHEC= Enterohemorrhagic Escherichia coli, VRSA= Vancomycin-resistant Staphylococcus aureus, CRE= Carbapenem-resistant Enterobacteriaceae, HFRS= Hemorrhagic fever with renal syndrome, CJD= Creutzfeldt-Jacob Disease, SFTS= Severe fever with thrombocytopenia syndrome.

Cum: Cumulative counts from 1st week to current week in a year.

* The reported data for year 2020, 2021 are provisional but the data from 2016 to 2019 are finalized data.

† According to surveillance data, the reported cases may include all of the cases such as confirmed, suspected, and asymptomatic carrier in the group.

‡ The reported surveillance data excluded no incidence data such as Ebola virus disease, Marburg Hemorrhagic fever, Lassa fever, Crimean Congo Hemorrhagic fever, South American Hemorrhagic fever, Rift Valley fever, Smallpox, Plague, Anthrax, Botulism, Tularemia, Newly emerging infectious disease syndrome, Severe Acute Respiratory Syndrome, Middle East Respiratory Syndrome, Human infection with zoonotic influenza, Novel Influenza, Diphtheria, Poliomyelitis, Haemophilus influenzae type b, Epidemic typhus, Rabies, Yellow fever, West Nile fever and Tick-borne Encephalitis.

Table 2. Reported cases of infectious diseases by geography, week ending April 10, 2021 (15th week)*

Unit: No. of cases[†]

Reporting area	Diseases of Category II											
	Tuberculosis			Varicella			Measles			Cholera		
	Current week	Cum. 2021	Cum. 5-year average [‡]	Current week	Cum. 2021	Cum. 5-year average [‡]	Current week	Cum. 2021	Cum. 5-year average [‡]	Current week	Cum. 2021	Cum. 5-year average [‡]
Overall	450	5,596	7,443	368	5,098	17,463	0	0	29	0	0	0
Seoul	74	905	1,337	27	680	1,946	0	0	3	0	0	0
Busan	26	368	514	16	343	1,012	0	0	1	0	0	0
Daegu	23	279	352	17	246	890	0	0	2	0	0	0
Incheon	14	284	398	26	281	908	0	0	1	0	0	0
Gwangju	12	142	194	12	194	680	0	0	0	0	0	0
Daejeon	12	130	163	12	141	476	0	0	3	0	0	0
Ulsan	5	99	146	6	92	482	0	0	0	0	0	0
Sejong	3	35	27	0	57	163	0	0	12	0	0	0
Gyeonggi	95	1,226	1,603	119	1,429	4,763	0	0	0	0	0	0
Gangwon	15	233	322	15	143	464	0	0	1	0	0	0
Chungbuk	14	181	231	5	151	442	0	0	0	0	0	0
Chungnam	22	291	353	19	196	675	0	0	1	0	0	0
Jeonbuk	25	226	295	22	225	704	0	0	1	0	0	0
Jeonnam	26	321	385	18	240	725	0	0	1	0	0	0
Gyeongbuk	47	446	543	14	239	973	0	0	2	0	0	0
Gyeongnam	28	365	479	35	354	1,649	0	0	1	0	0	0
Jeju	9	65	102	5	87	511	0	0	0	0	0	0

Cum: Cumulative counts from 1st week to current week in a year

* The reported data for year 2020, 2021 are provisional but the data from 2016 to 2019 are finalized data.

[†] According to surveillance data, the reported cases may include all of the cases such as confirmed, suspected, and asymptomatic carrier in the group.

[‡] Cum. 5-year average is mean value calculated by cumulative counts from 1st week to current week for 5 preceding years.

Table 2. (Continued) Reported cases of infectious diseases by geography, weeks ending April 10, 2021 (15th week)*

Unit: No. of cases[†]

Reporting area	Diseases of Category II											
	Typhoid fever			Paratyphoid fever			Shigellosis			Enterohemorrhagic <i>Escherichia coli</i>		
	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]
Overall	1	38	49	1	11	10	1	5	38	1	19	13
Seoul	0	1	11	0	0	2	0	0	8	0	3	3
Busan	0	5	5	0	4	1	0	0	2	0	0	0
Daegu	0	0	1	0	2	1	0	0	3	0	1	1
Incheon	0	1	4	0	0	1	0	0	3	0	1	1
Gwangju	0	1	1	0	0	0	0	0	1	0	1	1
Daejeon	0	2	2	0	0	0	0	0	1	0	1	0
Ulsan	0	0	2	0	0	0	0	0	1	0	0	0
Sejong	0	0	1	0	0	0	0	0	0	0	1	0
Gyeonggi	1	12	10	1	4	2	0	0	7	0	5	2
Gangwon	0	0	2	0	0	0	0	0	1	0	1	1
Chungbuk	0	0	2	0	0	0	0	0	1	0	0	0
Chungnam	0	1	2	0	0	0	0	0	2	0	0	0
Jeonbuk	0	0	0	0	0	1	0	1	1	0	0	1
Jeonnam	0	1	1	0	1	1	1	3	2	0	0	1
Gyeongbuk	0	4	2	0	0	0	0	0	4	0	2	0
Gyeongnam	0	10	3	0	0	1	0	0	1	0	2	1
Jeju	0	0	0	0	0	0	0	1	0	1	1	1

Cum: Cumulative counts from 1st week to current week in a year

* The reported data for year 2020, 2021 are provisional but the data from 2016 to 2019 are finalized data.

[†] According to surveillance data, the reported cases may include all of the cases such as confirmed, suspected, and asymptomatic carrier in the group.[§] Cum. 5-year average is mean value calculated by cumulative counts from 1st week to current week for 5 preceding years.

Table 2. (Continued) Reported cases of infectious diseases by geography, weeks ending April 10, 2021 (15th week)*

Unit: No. of cases[†]

Reporting area	Diseases of Category II											
	Viral hepatitis A			Pertussis			Mumps			Rubella		
	Current week	Cum. 2021	Cum. 5-year average [‡]	Current week	Cum. 2021	Cum. 5-year average [‡]	Current week	Cum. 2021	Cum. 5-year average [‡]	Current week	Cum. 2021	Cum. 5-year average [‡]
Overall	99	1,339	1,541	1	10	92	205	2,416	3,675	0	0	1
Seoul	26	290	273	0	1	15	20	275	399	0	0	0
Busan	2	22	60	0	0	4	10	149	220	0	0	0
Daegu	0	15	27	0	0	4	12	108	128	0	0	0
Incheon	4	99	114	1	1	8	9	111	169	0	0	0
Gwangju	2	28	27	0	0	5	13	83	165	0	0	0
Daejeon	2	40	149	0	0	3	5	78	99	0	0	0
Ulsan	1	9	12	0	0	2	7	77	126	0	0	0
Sejong	0	8	22	0	0	3	0	13	19	0	0	0
Gyeonggi	44	505	444	0	3	14	69	727	974	0	0	1
Gangwon	0	19	31	0	0	0	5	88	136	0	0	0
Chungbuk	3	46	65	0	1	2	5	49	97	0	0	0
Chungnam	7	106	121	0	0	2	11	108	161	0	0	0
Jeonbuk	4	54	61	0	0	3	7	94	166	0	0	0
Jeonnam	4	42	43	0	0	8	10	108	159	0	0	0
Gyeongbuk	0	29	36	0	3	8	14	120	190	0	0	0
Gyeongnam	0	12	48	0	1	10	7	181	416	0	0	0
Jeju	0	15	8	0	0	1	1	47	51	0	0	0

Cum: Cumulative counts from 1st week to current week in a year

* The reported data for year 2020, 2021 are provisional but the data from 2016 to 2019 are finalized data.

[†] According to surveillance data, the reported cases may include all of the cases such as confirmed, suspected, and asymptomatic carrier in the group.

[‡] Cum. 5-year average is mean value calculated by cumulative counts from 1st week to current week for 5 preceding years.

Table 2. (Continued) Reported cases of infectious diseases by geography, weeks ending April 10, 2021 (15th week)*

Unit: No. of cases[†]

Reporting area	Diseases of Category II						Diseases of Category III					
	Meningococcal disease			Scarlet fever			Tetanus			Viral hepatitis B		
	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]
Overall	0	0	4	13	229	3,681	0	7	3	6	117	97
Seoul	0	0	1	2	31	506	0	1	0	1	12	17
Busan	0	0	0	0	14	283	0	0	0	0	3	7
Daegu	0	0	0	1	3	112	0	2	0	1	3	3
Incheon	0	0	0	0	9	177	0	0	0	1	4	6
Gwangju	0	0	0	4	29	194	0	0	0	0	5	2
Daejeon	0	0	0	1	2	124	0	1	0	0	2	4
Ulsan	0	0	0	1	10	174	0	0	0	0	2	2
Sejong	0	0	0	0	0	17	0	0	0	0	0	0
Gyeonggi	0	0	1	2	63	1,020	0	1	0	2	45	25
Gangwon	0	0	1	0	4	45	0	0	0	0	3	3
Chungbuk	0	0	0	1	4	66	0	0	0	0	1	2
Chungnam	0	0	0	0	7	169	0	1	1	0	10	4
Jeonbuk	0	0	0	0	5	128	0	0	0	0	3	4
Jeonnam	0	0	0	1	12	154	0	0	1	0	7	4
Gyeongbuk	0	0	0	0	9	187	0	1	0	0	6	5
Gyeongnam	0	0	1	0	21	280	0	0	1	1	8	8
Jeju	0	0	0	0	6	45	0	0	0	0	3	1

Cum: Cumulative counts from 1st week to current week in a year

* The reported data for year 2020, 2021 are provisional but the data from 2016 to 2019 are finalized data.

† According to surveillance data, the reported cases may include all of the cases such as confirmed, suspected, and asymptomatic carrier in the group.

§ Cum. 5-year average is mean value calculated by cumulative counts from 1st week to current week for 5 preceding years.

Table 2. (Continued) Reported cases of infectious diseases by geography, weeks ending April 10, 2021 (15th week)*

Unit: No. of cases[†]

Reporting area	Diseases of Category III											
	Japanese encephalitis			Malaria			Legionellosis			<i>Vibrio vulnificus</i> sepsis		
	Current week	Cum. 2021	Cum. 5-year average [‡]	Current week	Cum. 2021	Cum. 5-year average [‡]	Current week	Cum. 2021	Cum. 5-year average [‡]	Current week	Cum. 2021	Cum. 5-year average [‡]
Overall	0	0	0	2	15	18	3	79	69	0	0	0
Seoul	0	0	0	0	1	6	1	12	21	0	0	0
Busan	0	0	0	0	1	0	0	2	4	0	0	0
Daegu	0	0	0	0	0	0	0	6	3	0	0	0
Incheon	0	0	0	1	1	2	0	2	5	0	0	0
Gwangju	0	0	0	0	0	1	0	1	1	0	0	0
Daejeon	0	0	0	0	0	0	0	1	1	0	0	0
Ulsan	0	0	0	0	0	0	0	2	1	0	0	0
Sejong	0	0	0	0	0	0	0	0	0	0	0	0
Gyeonggi	0	0	0	1	10	8	1	15	16	0	0	0
Gangwon	0	0	0	0	1	1	0	2	2	0	0	0
Chungbuk	0	0	0	0	0	0	0	2	2	0	0	0
Chungnam	0	0	0	0	1	0	0	1	2	0	0	0
Jeonbuk	0	0	0	0	0	0	0	8	2	0	0	0
Jeonnam	0	0	0	0	0	0	0	6	2	0	0	0
Gyeongbuk	0	0	0	0	0	0	0	1	5	0	0	0
Gyeongnam	0	0	0	0	0	0	1	4	2	0	0	0
Jeju	0	0	0	0	0	0	0	14	0	0	0	0

Cum: Cumulative counts from 1st week to current week in a year

* The reported data for year 2020, 2021 are provisional but the data from 2016 to 2019 are finalized data.

[†] According to surveillance data, the reported cases may include all of the cases such as confirmed, suspected, and asymptomatic carrier in the group.

[‡] Cum. 5-year average is mean value calculated by cumulative counts from 1st week to current week for 5 preceding years.

Table 2. (Continued) Reported cases of infectious diseases by geography, weeks ending April 10, 2021 (15th week)*

Unit: No. of cases[†]

Reporting area	Diseases of Category III											
	Murine typhus			Scrub typhus			Leptospirosis			Brucellosis		
	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]
Overall	0	3	0	13	183	189	5	24	8	0	2	0
Seoul	0	0	0	0	8	9	0	0	1	0	0	0
Busan	0	0	0	0	9	9	0	3	0	0	0	0
Daegu	0	0	0	0	8	1	0	0	0	0	0	0
Incheon	0	1	0	0	2	5	0	3	0	0	0	0
Gwangju	0	0	0	0	5	3	0	0	1	0	0	0
Daejeon	0	0	0	0	2	3	0	1	0	0	0	0
Ulsan	0	0	0	0	3	6	0	0	0	0	0	0
Sejong	0	0	0	0	0	1	0	0	0	0	0	0
Gyeonggi	0	1	0	2	10	17	1	2	2	0	2	0
Gangwon	0	0	0	0	2	5	2	5	0	0	0	0
Chungbuk	0	0	0	0	2	4	1	2	0	0	0	0
Chungnam	0	0	0	0	8	16	0	3	1	0	0	0
Jeonbuk	0	0	0	5	46	15	0	2	1	0	0	0
Jeonnam	0	0	0	3	48	44	1	2	1	0	0	0
Gyeongbuk	0	0	0	0	5	12	0	1	1	0	0	0
Gyeongnam	0	0	0	3	20	34	0	0	0	0	0	0
Jeju	0	1	0	0	5	5	0	0	0	0	0	0

Cum: Cumulative counts from 1st week to current week in a year

* The reported data for year 2020, 2021 are provisional but the data from 2016 to 2019 are finalized data.

[†] According to surveillance data, the reported cases may include all of the cases such as confirmed, suspected, and asymptomatic carrier in the group.

[§] Cum. 5-year average is mean value calculated by cumulative counts from 1st week to current week for 5 preceding years.

Table 2. (Continued) Reported cases of infectious diseases by geography, weeks ending April 10, 2021 (15th week)*

Unit: No. of cases[†]

Reporting area	Diseases of Category III											
	Hemorrhagic fever with renal syndrome			Creutzfeldt-Jacob Disease			Dengue fever			Q fever		
	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]
Overall	3	47	58	2	40	11	0	0	50	1	9	26
Seoul	0	1	3	1	5	3	0	0	15	0	1	1
Busan	0	0	1	0	4	0	0	0	4	0	0	1
Daegu	0	2	0	0	3	1	0	0	3	0	0	1
Incheon	0	1	1	0	3	0	0	0	3	0	0	0
Gwangju	0	2	1	0	1	0	0	0	0	0	0	1
Daejeon	0	0	0	0	1	0	0	0	0	0	0	1
Ulsan	0	0	0	0	0	0	0	0	1	0	0	1
Sejong	0	0	0	0	0	0	0	0	0	0	0	0
Gyeonggi	0	8	18	0	11	3	0	0	15	0	1	4
Gangwon	0	3	3	0	3	1	0	0	1	0	0	0
Chungbuk	0	1	3	0	0	0	0	0	1	0	0	5
Chungnam	0	8	5	1	2	0	0	0	2	1	5	3
Jeonbuk	1	11	5	0	2	1	0	0	0	0	0	3
Jeonnam	0	4	6	0	0	0	0	0	1	0	1	2
Gyeongbuk	2	4	8	0	1	1	0	0	1	0	1	1
Gyeongnam	0	2	3	0	3	1	0	0	2	0	0	2
Jeju	0	0	1	0	1	0	0	0	1	0	0	0

Cum: Cumulative counts from 1st week to current week in a year

* The reported data for year 2020, 2021 are provisional but the data from 2016 to 2019 are finalized data.

[†] According to surveillance data, the reported cases may include all of the cases such as confirmed, suspected, and asymptomatic carrier in the group.

[§] Cum. 5-year average is mean value calculated by cumulative counts from 1st week to current week for 5 preceding years.

Table 2. (Continued) Reported cases of infectious diseases by geography, weeks ending April 10, 2021 (15th week)*

Unit: No. of cases[†]

Reporting area	Diseases of Category IV								
	Lyme Borreliosis			Severe fever with thrombocytopenia syndrome			Zika virus infection		
	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]
Overall	0	0	1	0	1	0	0	0	–
Seoul	0	0	1	0	0	0	0	0	–
Busan	0	0	0	0	0	0	0	0	–
Daegu	0	0	0	0	0	0	0	0	–
Incheon	0	0	0	0	0	0	0	0	–
Gwangju	0	0	0	0	0	0	0	0	–
Daejeon	0	0	0	0	0	0	0	0	–
Ulsan	0	0	0	0	0	0	0	0	–
Sejong	0	0	0	0	0	0	0	0	–
Gyeonggi	0	0	0	0	0	0	0	0	–
Gangwon	0	0	0	0	0	0	0	0	–
Chungbuk	0	0	0	0	0	0	0	0	–
Chungnam	0	0	0	0	0	0	0	0	–
Jeonbuk	0	0	0	0	0	0	0	0	–
Jeonnam	0	0	0	0	0	0	0	0	–
Gyeongbuk	0	0	0	0	0	0	0	0	–
Gyeongnam	0	0	0	0	1	0	0	0	–
Jeju	0	0	0	0	0	0	0	0	–

Cum: Cumulative counts from 1st week to current week in a year

* The reported data for year 2020, 2021 are provisional but the data from 2016 to 2019 are finalized data.

[†] According to surveillance data, the reported cases may include all of the cases such as confirmed, suspected, and asymptomatic carrier in the group.

[§] Cum. 5-year average is mean value calculated by cumulative counts from 1st week to current week for 5 preceding years.

1. Influenza, Republic of Korea, weeks ending April 10, 2021 (15th week)

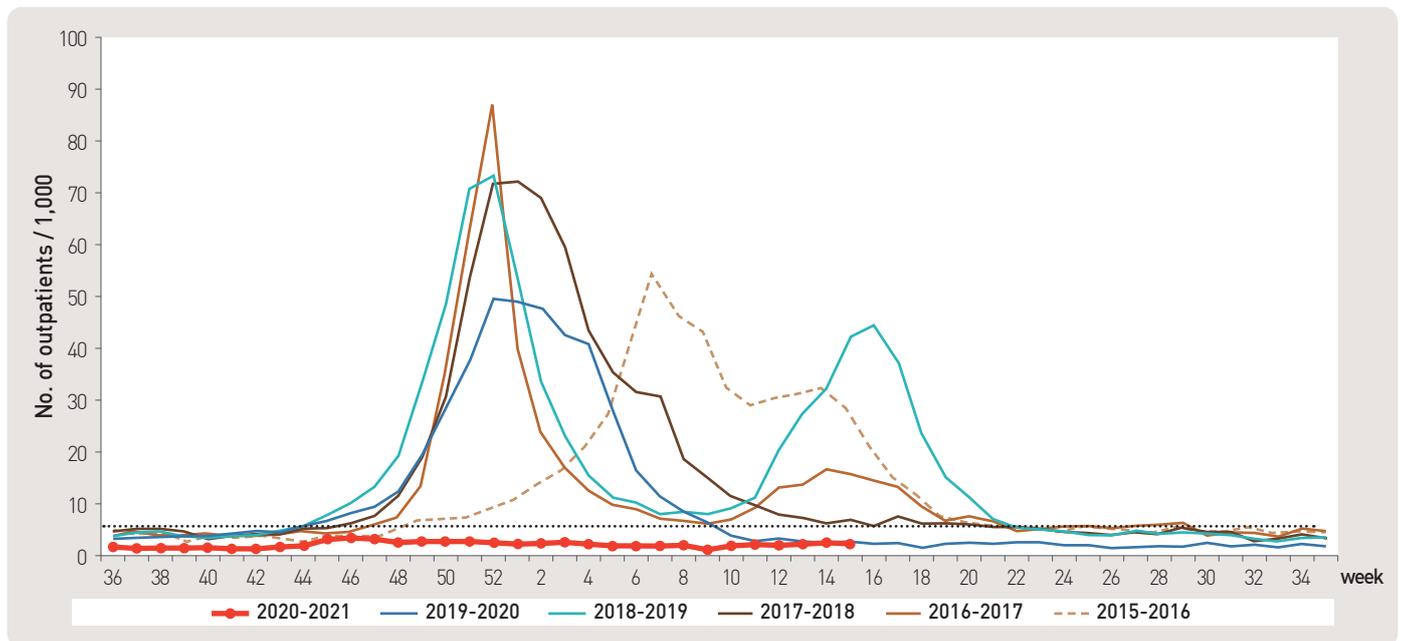


Figure 1. Weekly proportion of influenza-like illness per 1,000 outpatients, 2017-2018 to 2020-2021 flu seasons

2. Hand, Foot and Mouth Disease(HFMD), Republic of Korea, weeks ending April 10, 2021 (15th week)

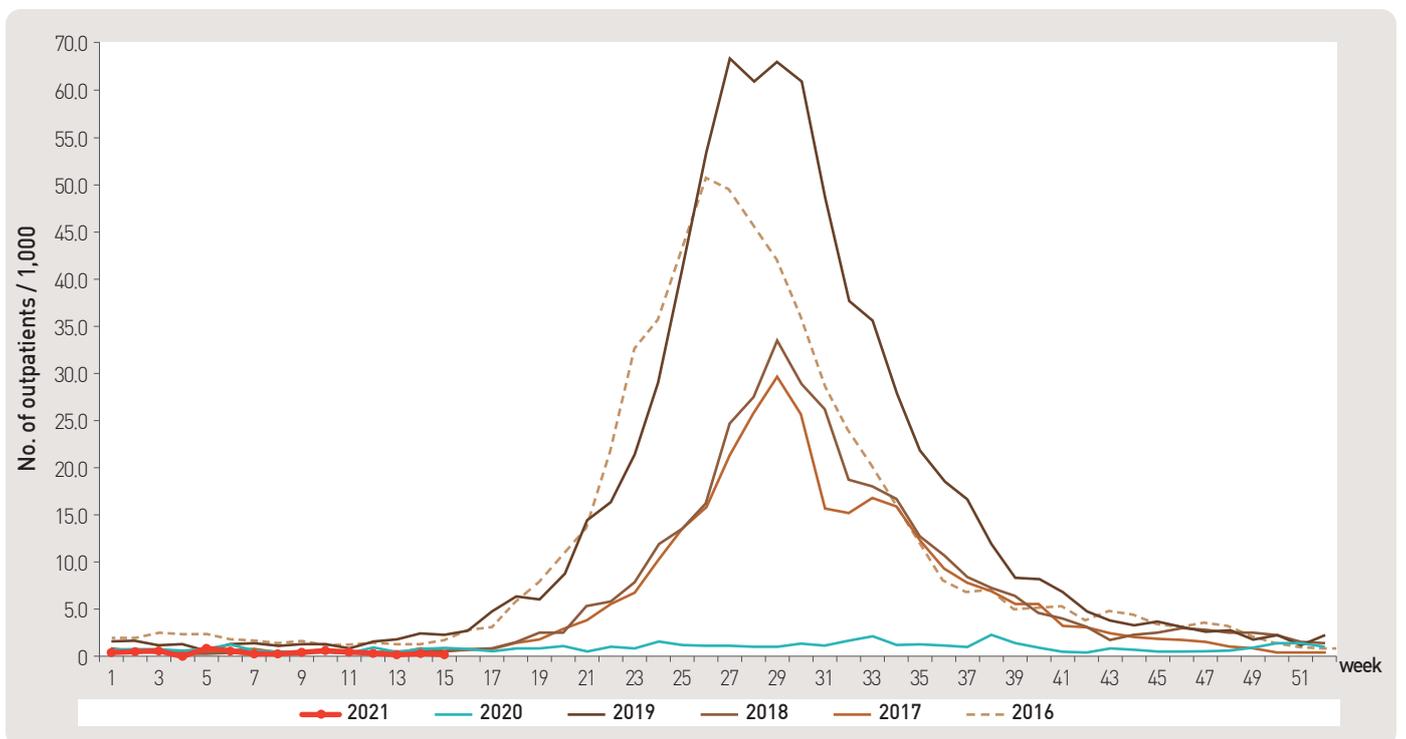


Figure 2. Weekly proportion of hand, foot and mouth disease per 1,000 outpatients, 2016-2021

3. Ophthalmologic infectious disease, Republic of Korea, weeks ending April 10, 2021 (15th week)

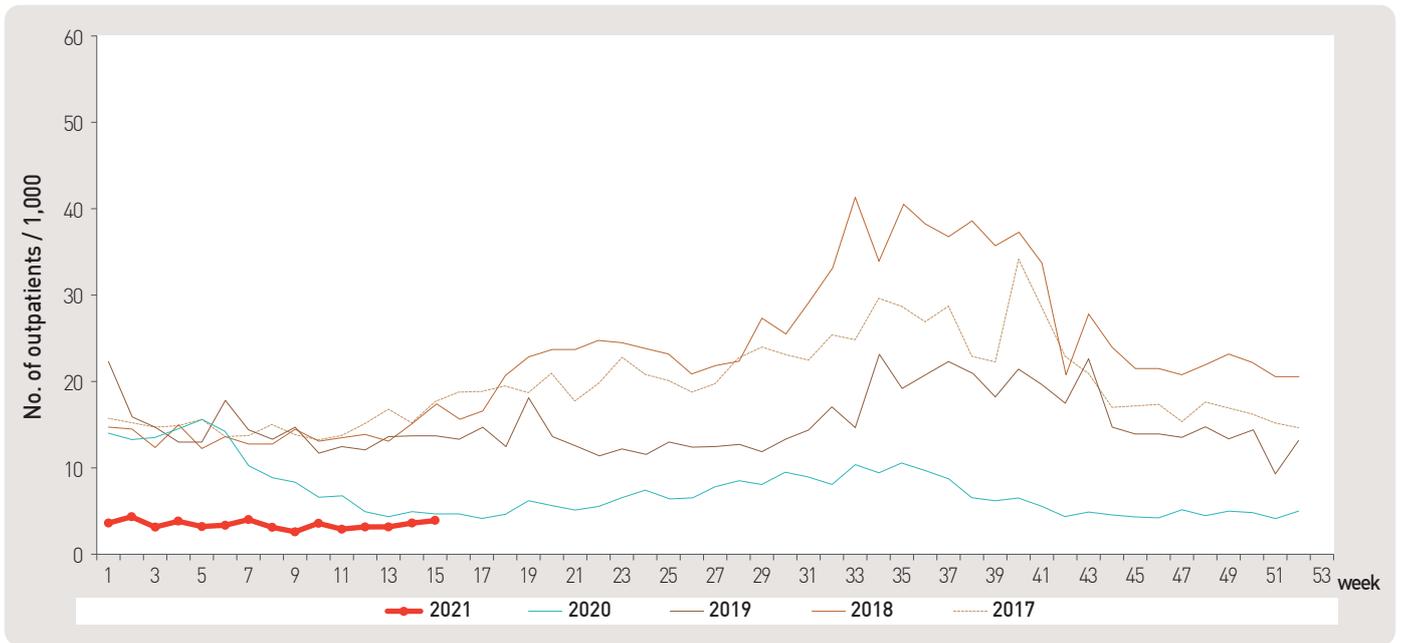


Figure 3. Weekly proportion of epidemic keratoconjunctivitis per 1,000 outpatients

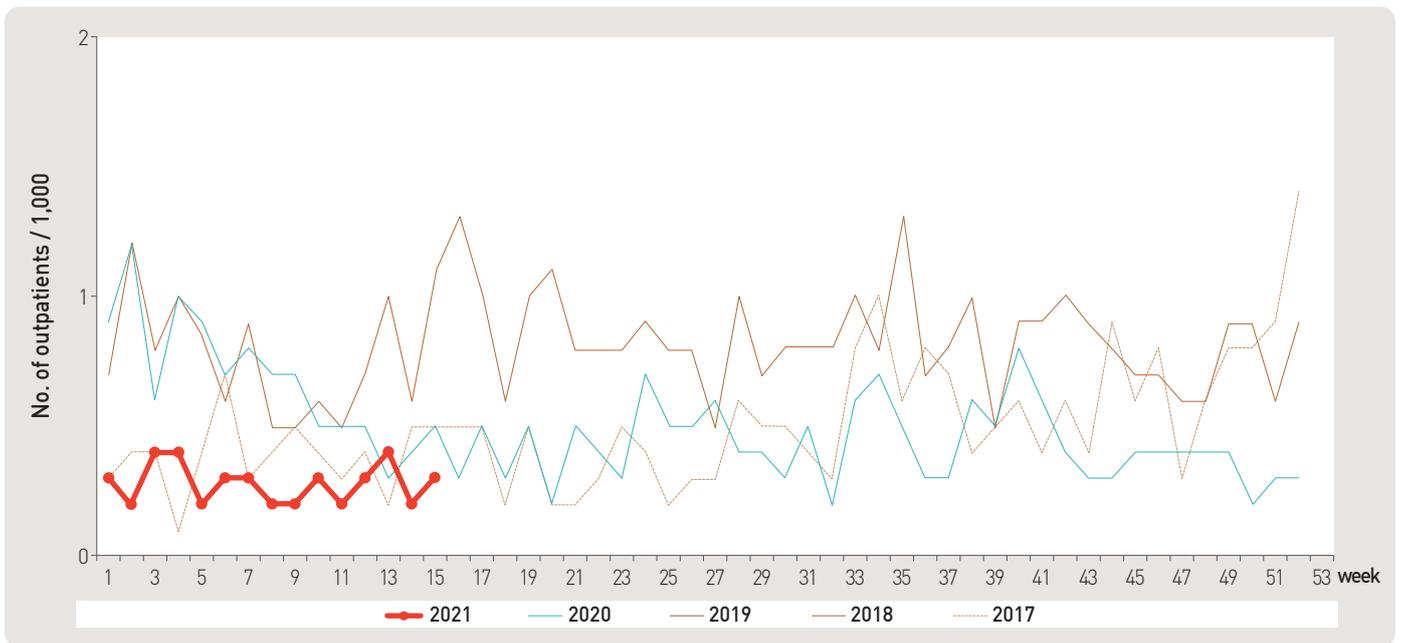


Figure 4. Weekly proportion of acute hemorrhagic conjunctivitis per 1,000 outpatients

4. Sexually Transmitted Diseases[†], Republic of Korea, weeks ending April 10, 2021 (15th week)

Unit: No. of cases/sentinels

Gonorrhea			Chlamydia			Genital herpes			Condyloma acuminata		
Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]
1.2	3.5	4.2	1.9	9.1	11.2	2.4	14.4	14.4	2.1	8.8	8.7

Human Papilloma virus infection			Primary			Syphilis Secondary			Congenital		
Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]	Current week	Cum. 2021	Cum. 5-year average [§]
3.8	33.1	4.9	1.0	1.4	0.3	1.0	1.4	0.3	0.0	1.0	0.2

Cum: Cumulative counts from 1st week to current week in a year

[†] According to surveillance data, the reported cases may include all of the cases such as confirmed, suspected, and asymptomatic carrier in the group.

[§] Cum. 5-year average is mean value calculated by cumulative counts from 1st week to current week for 5 preceding years.

▣ Waterborne and foodborne disease outbreaks, Republic of Korea, weeks ending April 10, 2021 (15th week)

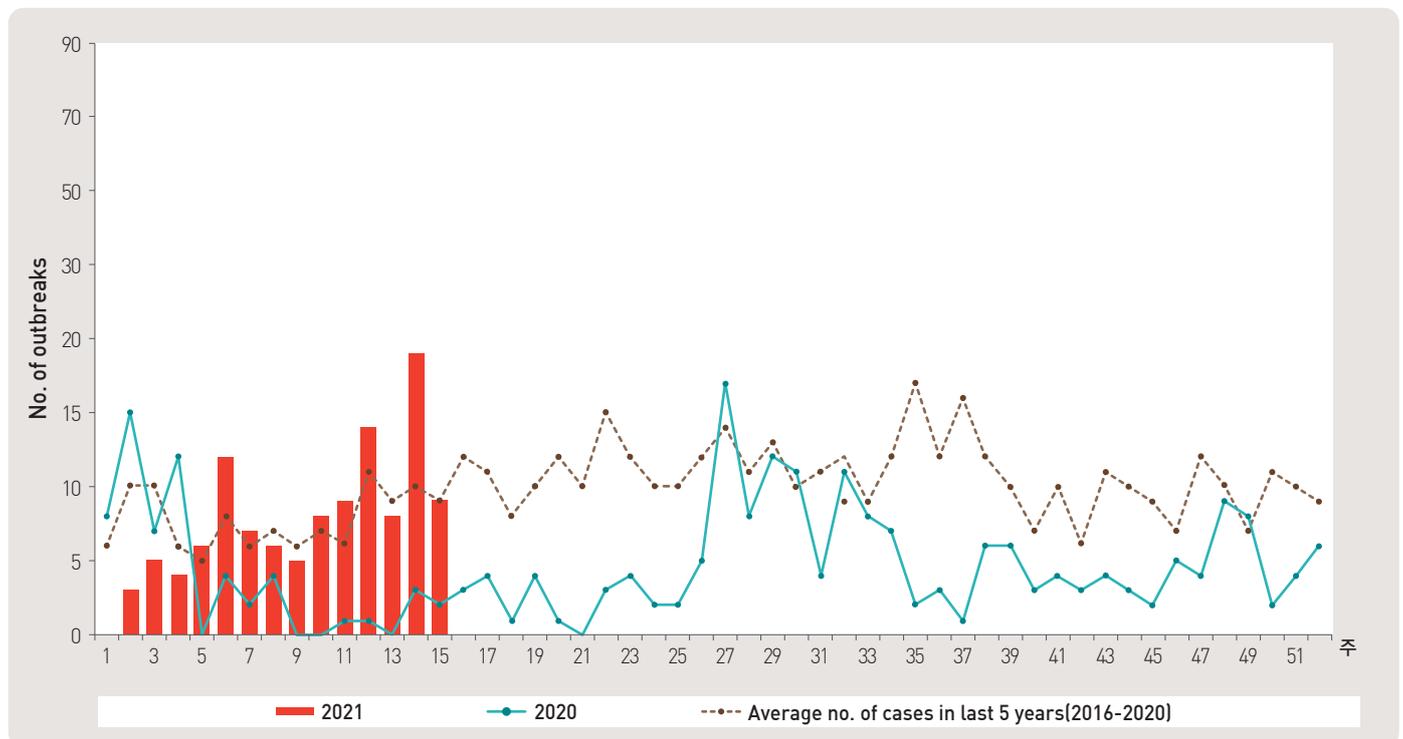


Figure 5. Number of waterborne and foodborne disease outbreaks reported by week, 2020–2021

1. Influenza viruses, Republic of Korea, weeks ending April 10, 2021 (15th week)

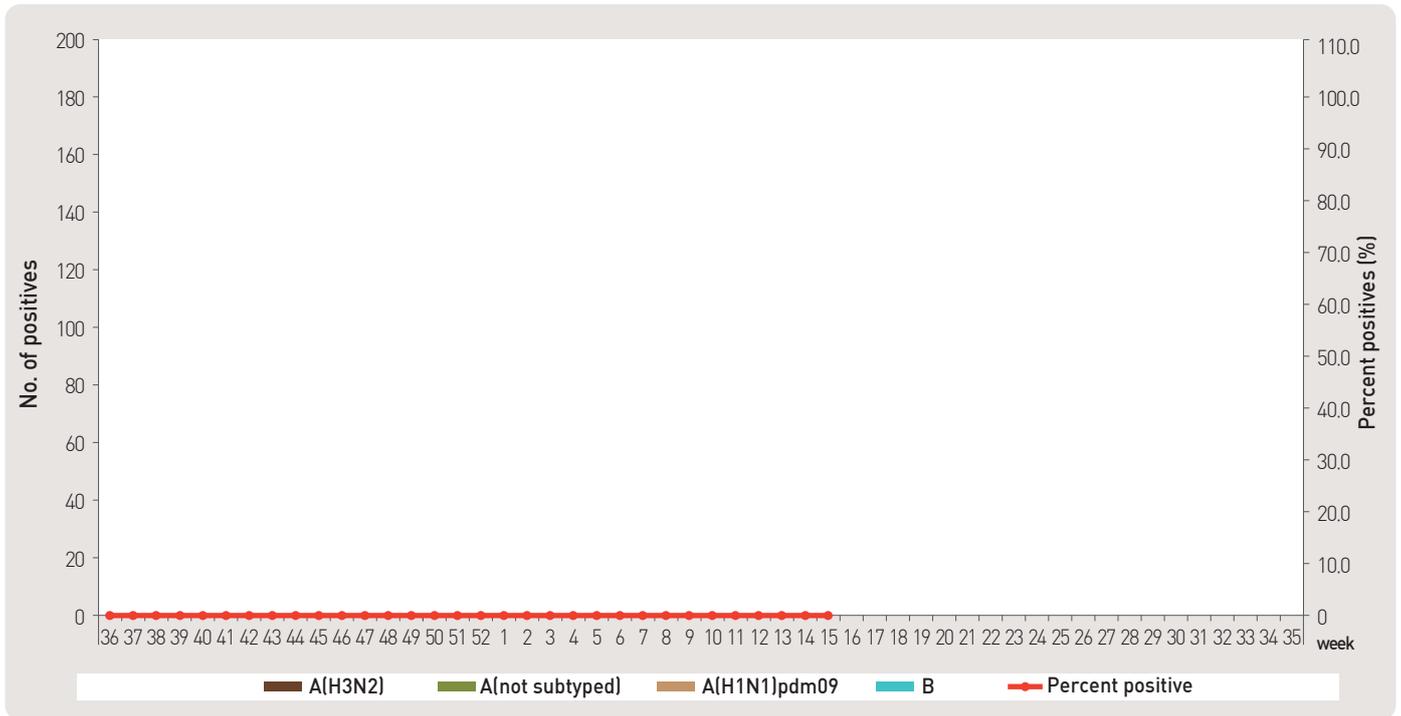


Figure 6. Number of specimens positive for influenza by subtype, 2020–2021 flu season

2. Respiratory viruses, Republic of Korea, weeks ending April 10, 2021 (15th week)

2021 (week)	Weekly total		Detection rate (%)							
	No. of samples	Detection rate (%)	HAdV	HPIV	HRSV	IFV	HCoV	HRV	HBoV	HMPV
12	112	63.4	7.1	0.0	0.0	0.0	0.0	49.1	7.1	0.0
13	109	64.2	2.8	0.0	0.0	0.0	0.0	48.6	12.8	0.0
14	109	55.0	4.6	0.0	0.0	0.0	0.0	42.2	8.3	0.0
15	122	66.4	6.6	0.0	0.0	0.0	0.0	47.5	12.3	0.0
Cum. ※	452	62.4	5.3	0.0	0.0	0.0	0.0	46.9	10.2	0.0
2020 Cum. ∇	5,819	48.6	6.5	0.4	3.1	12.0	3.4	18.4	3.5	1.4

– HAdV : human Adenovirus, HPIV : human Parainfluenza virus, HRSV : human Respiratory syncytial virus, IFV : Influenza virus,

HCoV : human Coronavirus, HRV : human Rhinovirus, HBoV : human Bocavirus, HMPV : human Metapneumovirus

※ Cum. : the rate of detected cases between March 14, 2021 – April 10, 2021 (Average No. of detected cases is 113 last 4 weeks)

∇ 2020 Cum. : the rate of detected cases between December 29, 2019 – December 26, 2020

▣ Acute gastroenteritis-causing viruses and bacteria, Republic of Korea, weeks ending April 3, 2021 (14th week)

◆ Acute gastroenteritis-causing viruses

Week	No. of sample	No. of detection (Detection rate, %)						
		Norovirus	Group A Rotavirus	Enteric Adenovirus	Astrovirus	Sapovirus	Total	
2021	11	65	19(29.2)	0(0.0)	0(0.0)	2(3.1)	0(0.0)	21(32.3)
	12	73	21(28.8)	0(0.0)	1(1.4)	5(6.8)	0(0.0)	27(37.0)
	13	73	24(32.9)	1(1.4)	0(0.0)	2(2.7)	0(0.0)	27(37.0)
	14	68	19(27.9)	2(2.9)	0(0.0)	5(7.4)	0(0.0)	26(38.2)
	Cum.	985	343(34.8)	20(2.0)	8(0.8)	15(1.5)	2(0.2)	388(39.4)

* The samples were collected from children ≤5 years of sporadic acute gastroenteritis in Korea.

◆ Acute gastroenteritis-causing bacteria

Week	No. of sample	No. of isolation (Isolation rate, %)										
		<i>Salmonella spp.</i>	Pathogenic <i>E.coli</i>	<i>Shigella spp.</i>	<i>V.parahaemolyticus</i>	<i>V. cholerae</i>	<i>Campylobacter spp.</i>	<i>C.perfringens</i>	<i>S. aureus</i>	<i>B. cereus</i>	Total	
2021	11	180	3 (1.7)	2 (1.1)	0 (0.0)	0 (0.0)	0 (0.0)	2 (1.1)	4 (2.2)	10 (5.6)	3 (1.7)	25 (13.9)
	12	204	4 (2.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	3 (1.5)	7 (3.4)	10 (4.9)	5 (2.5)	30 (14.7)
	13	205	4 (2.0)	2 (1.0)	1 (0.5)	0 (0.0)	0 (0.0)	1 (0.5)	6 (2.9)	8 (3.9)	1 (0.5)	23 (11.2)
	14	133	3 (2.3)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	2 (1.5)	1 (0.8)	3 (2.3)	4 (3.0)	14 (10.5)
	Cum.	2,690	32 (1.0)	35 (1.3)	1 (0.04)	0 (0.0)	0 (0.0)	25 (0.9)	61 (2.3)	99 (3.7)	36 (1.3)	293 (10.9)

* Bacterial Pathogens: *Salmonella spp.*, *E. coli* (*EHEC*, *ETEC*, *EPEC*, *EIEC*), *Shigella spp.*, *Vibrio parahaemolyticus*, *Vibrio cholerae*, *Campylobacter spp.*, *Clostridium perfringens*, *Staphylococcus aureus*, *Bacillus cereus*, *Listeria monocytogenes*, *Yersinia enterocolitica*.

* hospital participating in Laboratory surveillance in 2021(69 hospitals)

Enterovirus, Republic of Korea, weeks ending April 3, 2021 (14th week)

Aseptic meningitis

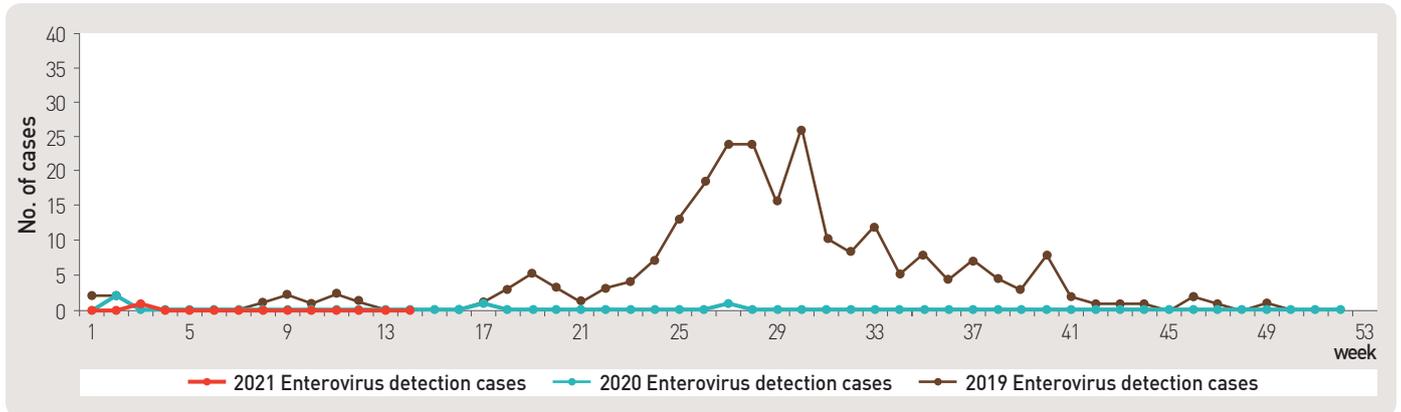


Figure 7. Detection case of enterovirus in aseptic meningitis patients from 2019 to 2021

HFMD and Herpangina

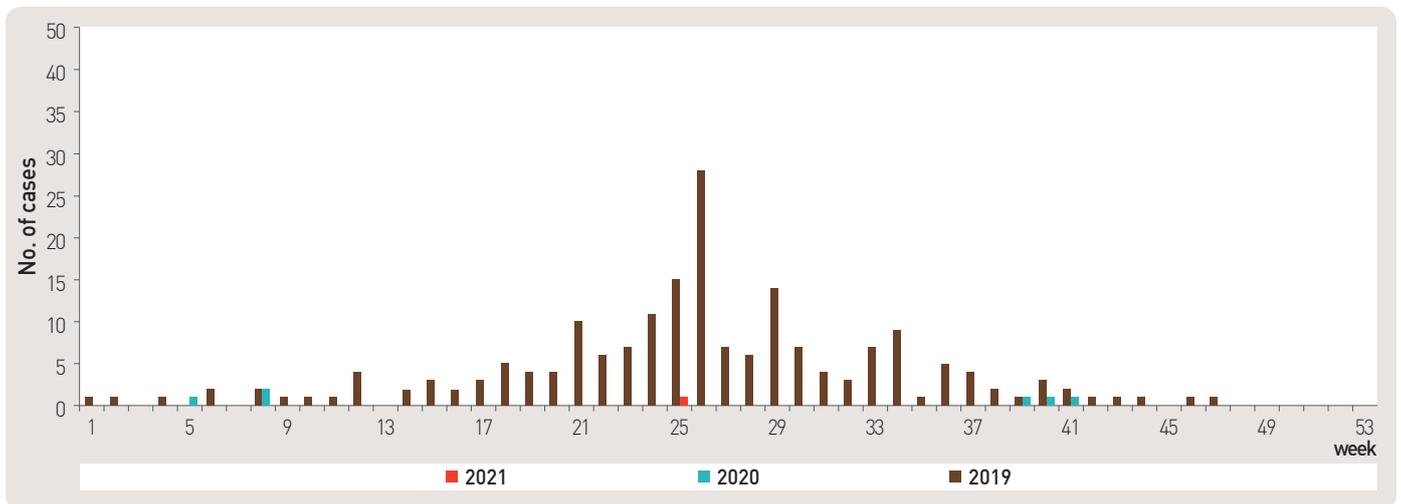


Figure 8. Detection case of enterovirus in HFMD and herpangina patients from 2019 to 2021

HFMD with Complications

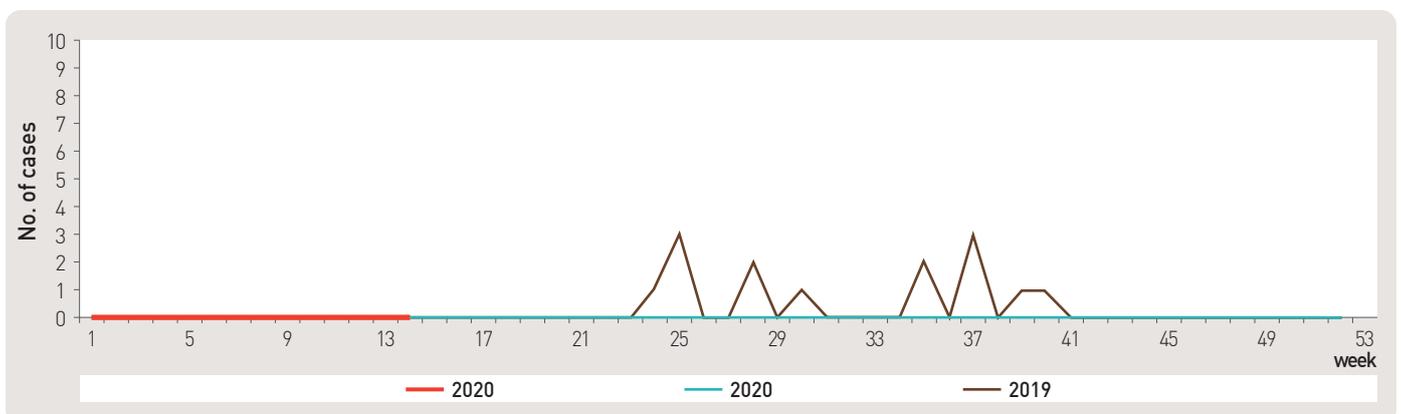


Figure 9. Detection case of enterovirus in HFMD with complications patients from 2019 to 2021

■ Vector surveillance / malaria vector mosquitoes, Republic of Korea, week ending April 3, 2021 (14th week)

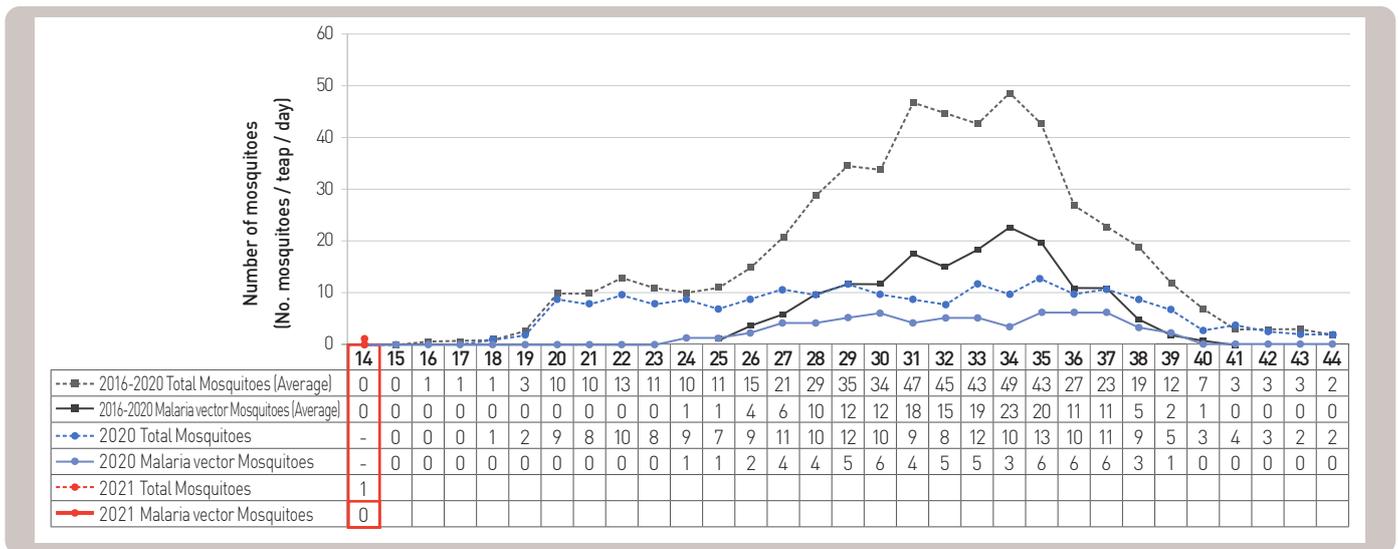


Figure 10. The weekly incidences of malaria vector mosquitoes in 2021

■ Vector surveillance / Japanese encephalitis vector mosquitoes, Republic of Korea, week ending April 10, 2021 (15th week)

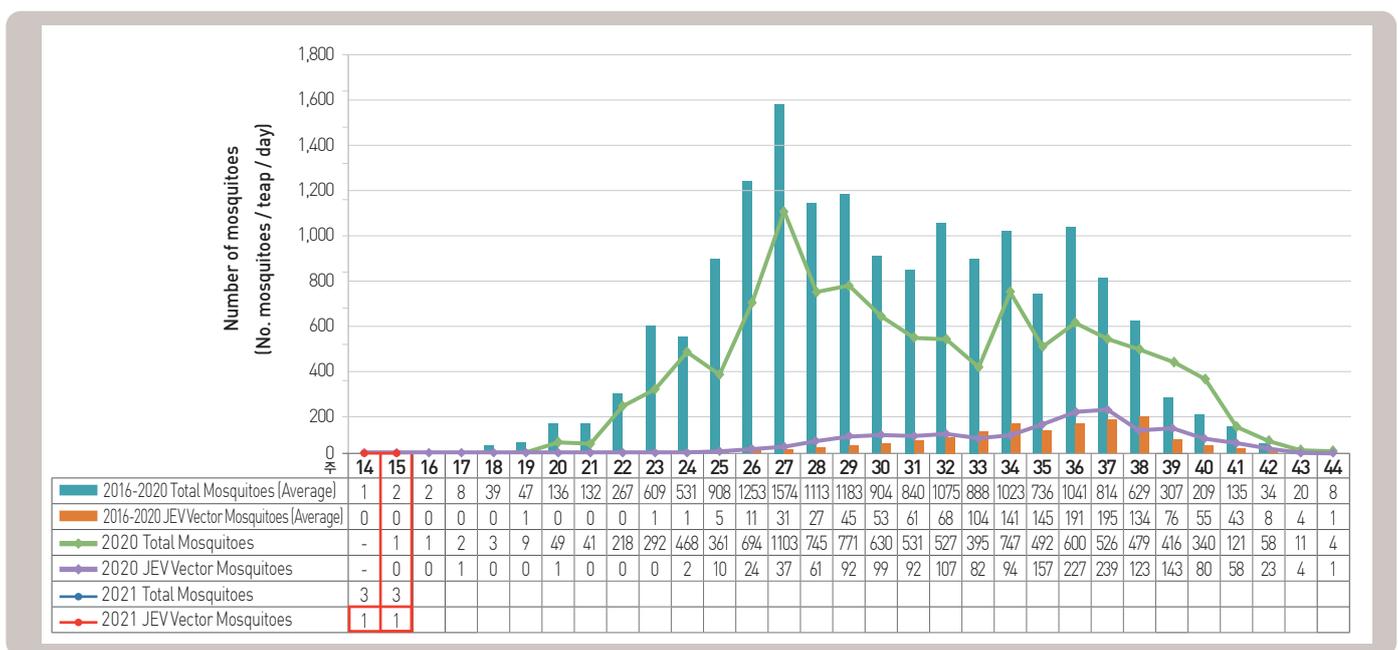


Figure 11. The weekly incidences of Japanese encephalitis vector mosquitoes in 2021

About PHWR Disease Surveillance Statistics

The Public Health Weekly Report (PHWR) Disease Surveillance Statistics is prepared by the Korea Disease Control and Prevention Agency (KDCA). These provisional surveillance data on the reported occurrence of national notifiable diseases and conditions are compiled through population-based or sentinel-based surveillance systems and published weekly, except for data on infrequent or recently-designated diseases. These surveillance statistics are informative for analyzing infectious disease or condition numbers and trends. However, the completeness of data might be influenced by some factors such as a date of symptom or disease onset, diagnosis, laboratory result, reporting of a case to a jurisdiction, or notification to Korea Disease Control and Prevention Agency. The official and final disease statistics are published in infectious disease surveillance yearbook annually.

Using and Interpreting These Data in Tables

- **Current Week** – The number of cases under current week denotes cases who have been reported to KDCA at the central level via corresponding jurisdictions(health centers, and health departments) during that week and accepted/approved by surveillance staff.
- **Cum. 2021** – For the current year, it denotes the cumulative(Cum) year-to-date provisional counts for the specified condition.
- **5-year weekly average** – The 5-year weekly average is calculated by summing, for the 5 preceding years, the provisional incidence counts for the current week, the two weeks preceding the current week, and the two weeks following the current week. The total sum of cases is then divided by 25 weeks. It gives help to discern the statistical aberration of the specified disease incidence by comparing difference between counts under current week and 5-year weekly average.

For example,

* 5-year weekly average for current week= $(X1 + X2 + \dots + X25) / 25$

	10	11	12	13	14
2021			Current week		
2020	X1	X2	X3	X4	X5
2019	X6	X7	X8	X9	X10
2018	X11	X12	X13	X14	X15
2017	X16	X17	X18	X19	X20
2016	X21	X22	X23	X24	X25

- **Cum. 5-year average** – Mean value calculated by cumulative counts from 1st week to current week for 5 preceding years. It gives help to understand the increasing or decreasing pattern of the specific disease incidence by comparing difference between cum. 2021 and cum. 5-year average.

Contact Us

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